

Db 61 GACCACTTTGAATTTTGGAGCCATTGGGAAGSCAGTTTTGGGAAGTCTGCATTGTA 120
Qy 121 CAGAGAATGATACCAAGAAGATGTACGCAATGAAGTACATGAATAAACAAGTGCCTG 180
Db 121 CAGAGAATGATACCAAGAAGATGTACGCAATGAAGTACATGAATAAACAAGTGCCTG 180
Qy 181 GAGCGCAATGAAGTGAAGAAATGCTTCAAGNACTCCAGATCATCGAGGCTCGAGCAC 240
Db 181 GAGCGCAATGAAGTGAAGAAATGCTTCAAGNACTCCAGATCATCGAGGCTCGAGCAC 240
Qy 241 CTTTCTCTGTTAAATTTGTTGGTATTCTTCAAGATGAGGAAGACATGTTCAATGTTG 300
Db 241 CTTTCTCTGTTAAATTTGTTGGTATTCTTCAAGATGAGGAAGACATGTTCAATGTTG 300
Qy 301 GACCTCTGCTGGGTGAGACCTGGTATTATCACTGCAAGAAAGCTCCACTTCAAGGAA 360
Db 301 GACCTCTGCTGGGTGAGACCTGGTATTATCACTGCAAGAAAGCTCCACTTCAAGGAA 360
Qy 361 GAAACAGTGAAGCTTCTATCTGTGAGCTGTGATGGCCCTGGATCACTCTGAGAACAG 420
Db 361 GAAACAGTGAAGCTTCTATCTGTGAGCTGTGATGGCCCTGGATCACTCTGAGAACAG 420
Qy 421 GGCATCATTCACAGGATATGAAGCTGCACATATTTTACTTGACGAACATGGGCAGTG 480
Db 421 GGCATCATTCACAGGATATGAAGCTGCACATATTTTACTTGACGAACATGGGCAGTG 480
Qy 481 CACATCAGAGATTTCAACATTTCTGCGATGCTGCCAGGGAGACACAGATTACCAACATG 540
Db 481 CACATCAGAGATTTCAACATTTCTGCGATGCTGCCAGGGAGACACAGATTACCAACATG 540
Qy 541 GGTGCAACAGCCTTACATGCGACCTGAGATGTTTCACTTCAGAAAAGGAGCGGCTAT 600
Db 541 GGTGCAACAGCCTTACATGCGACCTGAGATGTTTCACTTCAGAAAAGGAGCGGCTAT 600
Qy 601 TCTTTGCTGTTGACTGTGTTGCTGCGAGTGCAGGATATGACTCTGAGAGCGCG 660
Db 601 TCTTTGCTGTTGACTGTGTTGCTGCGAGTGCAGGATATGACTCTGAGAGCGCG 660
Qy 661 AGACGATATCATATTCGCTCCAGTACTTCCAGAGGAAATTTGATACACAGCTTTGAGACG 720
Db 661 AGACGATATCATATTCGCTCCAGTACTTCCAGAGGAAATTTGATACACAGCTTTGAGACG 720
Qy 721 ACTGTTGTAACCTTACCTTCTGCTGCTGATCAGGAAATGGTGTCACTTCTTAAAGGTA 780
Db 721 ACTGTTGTAACCTTACCTTCTGCTGCTGATCAGGAAATGGTGTCACTTCTTAAAGGTA 780
Qy 781 CTCGAACCTTATCCAGACCAAGATTTTCTGATTTATGATGTCAGAACTTCCCGTAT 840
Db 781 CTCGAACCTTATCCAGACCAAGATTTTCTGATTTATGATGTCAGAACTTCCCGTAT 840
Qy 841 ATGAATGATATAAATCTGGGATGCACTTTTTCAGAGAGGCTCATTCAGAGTTTCACTTCT 900
Db 841 ATGAATGATATAAATCTGGGATGCACTTTTTCAGAGAGGCTCATTCAGAGTTTCACTTCT 900
Qy 901 AATAAGGAGGCTGAATTTGATGCTTCACTTTGAACTTTGAGGAAATGATTTTGAGTCC 960
Db 901 AATAAGGAGGCTGAATTTGATGCTTCACTTTGAACTTTGAGGAAATGATTTTGAGTCC 960
Qy 961 AAACCTCTACATAAGAAAAGGCTGTCGCAAGAGGAGAGGATATCAGGAAATGC 1020
Db 961 AAACCTCTACATAAGAAAAGGCTGTCGCAAGAGGAGAGGATATCAGGAAATGC 1020
Qy 1021 GATTTCTCTCAGACATGCTTCTTCAAGAGACCTTTGATCTCTGTCAGAGAGGATTCATA 1080
Db 1021 GATTTCTCTCAGACATGCTTCTTCAAGAGACCTTTGATCTCTGTCAGAGAGGATTCATA 1080
Qy 1081 ATTTTCAAGAGAAAAGTAAACAGGACTTTTAAACAAAGACCAACCAAACTAGCCTTG 1140
Db 1081 ATTTTCAAGAGAAAAGTAAACAGGACTTTTAAACAAAGACCAACCAAACTAGCCTTG 1140
Qy 1141 GAAACAAACCAAGACCCCAAGAGTGAACAAATGGACA 1183
Db 1141 GAAACAAACCAAGACCCCAAGAGTGAACAAATGGACA 1183

RESULT 7

US-10-288-798-44
; Sequence 44, Application US/10288798
; Publication No. US20030207299A1
; GENERAL INFORMATION:
; APPLICANT: BANDMAN, Olga; NGUYEN, Damiel B;
; APPLICANT: WALIA, Navinder K.; HAPALIA, April J.A.;
; APPLICANT: YAO, Monique G.; GANDHI, Ameena R.;
; APPLICANT: GURURAJAN, Rajagopal; DING, Li;
; APPLICANT: PATTERSON, Chandra; YUE, Henry;
; APPLICANT: BAUGHN, Marian R.; TRIBOULEY, Vicki S.;
; APPLICANT: THORNTON, Michael; ELLIOTT, Craig H.;
; APPLICANT: LU, Yan; ISON, Craig H.;
; APPLICANT: AZIMZAI, Valda; BURRILL, John D.;
; APPLICANT: MARCUS, Gregory A.; ZINGLER, Kurt A.;
; APPLICANT: LU, Dyung Aina M.; LAL, Preeti G.;
; APPLICANT: RAMKUMAR, Jayalaxmi; WARREN, Bridget A.;
; APPLICANT: KEARNEY, Liam; POLICKY, Jennifer L.;
; APPLICANT: THANGAVELU, Kavitha; BURFORD, Neil
; TITLE OF INVENTION: HUMAN KINASES
; FILE REFERENCE: PI-0209 USA
; CURRENT APPLICATION NUMBER: US/10/288,798
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: PCT/US01/27219
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/240,542
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: US 60/238,389
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 60/236,499
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: US 60/234,902
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US 60/232,654
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US 60/231,357
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: US 60/229,873
; PRIOR FILING DATE: 2000-08-31
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PERL Program
; SEQ ID NO 44
; LENGTH: 1594
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No. US20030207299A1 7946584CB1
US-10-288-798-44

Query Match 95.2%; Score 1165.4; DB 15; Length 1594;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 1172; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 1 ATGGAGCCCAACACTTCAAGAAACCAACCAAGTGTTCATGAAATGAAGATGTCAACTTT 60
Db 404 ATGGAGCCCAACACTTCAAGAAACCAACCAAGTGTTCATGAAATGAAGATGTCAACTTT 463
Qy 61 GACCACCTTTGAAATTTTTCGAGCCATTGGGAAAGGCAAGTTTGGGAAAGGTCGCAATTGTA 120
Db 464 GACCACCTTTGAAATTTTTCGAGCCATTGGGAAAGGCAAGTTTGGGAAAGGTCGCAATTGTA 523
Qy 121 CAGNAGAAATGATACCAAGAAGATGTACGCAATGAAGTACATGAATAAACAAGTGCCTG 180
Db 524 CAGNAGAAATGATACCAAGAAGATGTACGCAATGAAGTACATGAATAAACAAGTGCCTG 583
Qy 181 GAGCGCAATGAAGTGAAGAAATGCTTCAAGGAACTCCAGATCATCGAGGCTCTGGAGCAC 240
Db 584 GAGCGCAATGAAGTGAAGAAATGCTTCAAGGAACTCCAGATCATCGAGGCTCTGGAGCAC 643

Db 764 GAAACAGTGAAGCTCTTCATCTGTGAGCTGGTCTATGGCCCTGGACTCCTGACAGAACCG 823
Qy 421 CGCATCATTCACAGGATATGAAGCTGCAATATTTTACTTGGACGAACATGGGACGCTG 480
Db 824 CGCATCATTCACAGGATATGAAGCTGCAATATTTTACTTGGACGAACATGGGACGCTG 883
Qy 481 CACATCACAGATTTCAACATTTCTGCGATGCTGCCAGGAGACACAGATTTACACCATG 540
Db 884 CACATCACAGATTTCAACATTTCTGCGATGCTGCCAGGAGACACAGATTTACACCATG 943
Qy 541 GCTGGCACCAGCCTTACATGCACTGAGATGTTGAGCTCCAGAAAAGGAGCAGGCTAT 600
Db 944 GCTGGCACCAGCCTTACATGCACTGAGATGTTGAGCTCCAGAAAAGGAGCAGGCTAT 1003
Qy 601 TCCCTTGTCTGCTGACTGGTGGTCCCTGGGAGTGACGGCATATGAACCTGCTGAGAGCCGG 660
Db 1004 TCCCTTGTCTGCTGACTGGTGGTCCCTGGGAGTGACGGCATATGAACCTGCTGAGAGCCGG 1063
Qy 661 AGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAAATTTGTACACACGTTTGAGAGC 720
Db 1064 AGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAAATTTGTACACACGTTTGAGAGC 1123
Qy 721 ACTGTTGTAACTTACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
Db 1124 ACTGTTGTAACTTACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1183
Qy 781 CTGGAACCTTAATCCAGACCAACGATTTTCTCAGTTATCTGATGTCAGAACTTCCCGTAT 840
Db 1184 CTGGAACCTTAATCCAGACCAACGATTTTCTCAGTTATCTGATGTCAGAACTTCCCGTAT 1243
Qy 841 ATGAATGATATAAATCGGATGAGCTTTTTCAGAAAGGCTCATTTCCAGGTTTCAATTCCT 900
Db 1244 ATGAATGATATAAATCGGATGAGCTTTTTCAGAAAGGCTCATTTCCAGGTTTCAATTCCT 1303
Qy 901 ANTAAGGCAGCTGAATTTGTATGATCTTACCTTTGAACTTGAGGAATGATTTTGAGTCC 960
Db 1304 ANTAAGGCAGCTGAATTTGTATGATCTTACCTTTGAACTTGAGGAATGATTTTGAGTCC 1363
Qy 961 AACCTCTACATAAGAAAAAAGGCTCTGGCAAGAGGAGGATATGAGGAATGC 1020
Db 1364 AACCTCTACATAAGAAAAAAGGCTCTGGCAAGAGGAGGATATGAGGAATGC 1423
Qy 1021 GATTTCTTCAGACATGCTTCTTCAAGAGCAGCTTGAATCTGTCAGAGAGGAGTTTCATA 1080
Db 1424 GATTTCTTCAGACATGCTTCTTCAAGAGCAGCTTGAATCTGTCAGAGAGGAGTTTCATA 1483
Qy 1081 ATTTTCAACAGAAAGATTAACAGGAGCTTTTAACAAAGACACCAAAATCTAGCCTTG 1140
Db 1484 ATTTTCAACAGAAAGATTAACAGGAGCTTTTAACAAAGACACCAAAATCTAGCCTTG 1543
Qy 1141 GAAACAAACCAAGACCCACAGTGCATAATGGACAAATGGACA 1183
Db 1544 GAACAAACCAAGACCCACAGTGCATGAGTGGTCAAGATAACA 1586

RESULT 9

US-10-182-243-1
; Sequence 1, Application US/10182243
; Publication No. US20040048310A1
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY D.
; APPLICANT: WHYTE, DAVID
; APPLICANT: MANNING, GERARD
; APPLICANT: SUDARSANAM, SUCHA
; APPLICANT: MARTINEZ, RICARDO
; TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES AND PROTEIN KINASE-LIKE
; TITLE OF INVENTION: ENZYMES
; FILE REFERENCE: 038602/1366
; CURRENT APPLICATION NUMBER: US/10/182,243
; CURRENT FILING DATE: 2003-07-07
; PRIOR APPLICATION NUMBER: PCT/US01/02337
; PRIOR FILING DATE: 2001-01-25

; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1594
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-182-243-1
Query Match 95.2%; Score 1165.4; DB 16; Length 1594;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 1172; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
Qy 1 ATGGAGCCCAACACTTCAAGAAAAACCACAGTGTGTTGATGAAAAATGAAGATGTCAACTTT 60
Db 404 ATGGAGCCCAACACTTCAAGAAAAACCACAGTGTGTTGATGAAAAATGAAGATGTCAACTTT 463
Qy 61 GACCACTTTGAAATTTTGGAGCCCAATTTGGGAAAGGCGAGTTTGGGAAAGGCTCTGCAATTGTA 120
Db 464 GACCACTTTGAAATTTTGGAGCCCAATTTGGGAAAGGCGAGTTTGGGAAAGGCTCTGCAATTGTA 523
Qy 121 CAGAAAGATGATACCAAGAAAGATGTACGCAATGAAGTACATGAATAAACAAGTGGCGTG 180
Db 524 CAGAAAGATGATACCAAGAAAGATGTACGCAATGAAGTACATGAATAAACAAGTGGCGTG 583
Qy 181 GAGCGCAATGAAGTGAAGAAATGTTCTCAAGAACTCCAGATCATGCAAGGCTCTGGAGCAC 240
Db 584 GAGCGCAATGAAGTGAAGAAATGTTCTCAAGAACTCCAGATCATGCAAGGCTCTGGAGCAC 643
Qy 241 CCTTCTCTGTTAAATTTTGGTATTCTTCCAGATGAGGAGACATGTTCAATGTTGGTG 300
Db 644 CCTTCTCTGTTAAATTTTGGTATTCTTCCAGATGAGGAGACATGTTCAATGTTGGTG 703
Qy 301 GACCTCTGCTGGTGGAGACCTTGCCTTATCCTGCAACAGAACCTCCACTTCAAGGAA 360
Db 704 GACCTCTGCTGGTGGAGACCTTGCCTTATCCTGCAACAGAACCTCCACTTCAAGGAA 763
Qy 361 GAAACAGTGAAGCTTTCATCTGAGCTGGTCAAGCTGATGCTGCAAGGAGACACAGATTTACCCATG 420
Db 764 GAAACAGTGAAGCTTTCATCTGAGCTGGTCAAGCTGATGCTGCAAGGAGACACAGATTTACCCATG 823
Qy 421 CGCATCATTCACAGGATATGAAGCTTGAAGCTTGAACATATTTTACTTGCAGAACATGGGCACTG 480
Db 824 CGCATCATTCACAGGATATGAAGCTTGAAGCTTGAACATATTTTACTTGCAGAACATGGGCACTG 883
Qy 481 CACATCACAGATTTCAACATTTGCTGCGATGCTGCCAGGAGACACAGATTTACCCATG 540
Db 884 CACATCACAGATTTCAACATTTGCTGCGATGCTGCCAGGAGACACAGATTTACCCATG 943
Qy 541 GCTGGCACCAGCCTTACATGCACTGAGATGTTGAGCTCCAGAAAAGGAGCAGGCTAT 600
Db 944 GCTGGCACCAGCCTTACATGCACTGAGATGTTGAGCTCCAGAAAAGGAGCAGGCTAT 1003
Qy 601 TCCCTTGTCTGCTGACTGGTGGTCCCTGGGAGTGACGGCATATGAACCTGCTGAGAGCCGG 660
Db 1004 TCCCTTGTCTGCTGACTGGTGGTCCCTGGGAGTGACGGCATATGAACCTGCTGAGAGCCGG 1063
Qy 661 AGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAAATTTGTACACACGTTTGAGAGC 720
Db 1064 AGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAAATTTGTACACACGTTTGAGAGC 1123
Qy 721 ACTGTTGTAACTTACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
Db 1124 ACTGTTGTAACTTACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1183
Qy 781 CTGGAACCTTAATCCAGACCAACGATTTTCTCAGTTATCTGATGTCAGAACTTCCCGTAT 840
Db 1184 CTGGAACCTTAATCCAGACCAACGATTTTCTCAGTTATCTGATGTCAGAACTTCCCGTAT 1243
Qy 841 ATGAATGATATAAATCGGATGAGCTTTTTCAGAAAGGCTCATTTCCAGGTTTCAATTCCT 900
Db 1244 ATGAATGATATAAATCGGATGAGCTTTTTCAGAAAGGCTCATTTCCAGGTTTCAATTCCT 1303
Qy 901 ANTAAGGCAGCTGAATTTGTATGATCTTACCTTTGAACTTGAGGAATGATTTTGAGTCC 960

Db 1304 AATAAGGCGAGCTGAATGTGATCTTACCTTTGACCTTTGAGGAATGATTTTGAGATCC 1363
Qy 961 AAACCTCTACATAAGAAAAAAGCGTCTGCAAGAGGAGGAGGATATGAGGAATGC 1020
Db 1364 AAACCTCTACATAAGAAAAAAGCGTCTGCAAGAGGAGGAGGATATGAGGAATGC 1423
Qy 1021 GATTCCTCTCAGACATGCTCTCTCAAGAGACACCTTGACTCTGCTCCAGAGGAGTTCCATA 1080
Db 1424 GATTCCTCTCAGACATGCTCTCTCAAGAGACACCTTGACTCTGCTCCAGAGGAGTTCCATA 1483
Qy 1081 ATTTTCAACAGAGAAAAAGTAAACAGGACCTTTTAAACAAAGACCAACCAAACTAGCCTTG 1140
Db 1484 ATTTTCAACAGAGAAAAAGTAAACAGGACCTTTTAAACAAAGACCAACCAAACTAGCCTTG 1543
Qy 1141 GAAACCAACCAAGACCCCAAGTGAACAAATGGACAAATGGACA 1183
Db 1544 GAAACCAACCAAGACCCCAAGTGAACAAATGGACAAATGGACA 1586

RESULT 10

US-10-410-764-102
; Sequence 102, Application US/10410764
; Publication No. US20040005664A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Meyers, Rachel E.
; APPLICANT: MacBeth, Kyle J.
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Rudolph-Owen, Laura A.
; APPLICANT: Weich, Nadine S.
; APPLICANT: Olandt, Peter J.
; APPLICANT: Tsai, Fong-Ying
; APPLICANT: Kapeller-Liebermann, Rosana
; APPLICANT: Carroll, Joseph M.
; TITLE OF INVENTION: 26199, 33530, 33949, 47148, 50226,
; TITLE OF INVENTION: 58764, 62113, 32144, 32235, 23565, 13305, 14911, 86216,
; TITLE OF INVENTION: 25206 AND 8843 MOLECULES AND USES THEREFOR
; FILE REFERENCE: MPI03-0520MNM
; CURRENT APPLICATION NUMBER: US/10/410,764
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: US 09/924,358
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/229,300
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: US 10/350,553
; PRIOR FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: US 60/351,572
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: US 09/966,614
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US 60/238,054
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: US 10/281,094
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US 60/347,815
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 10/076,535
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US 60/269,440
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 102
; LENGTH: 1191
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)....(1191)
US-10-410-764-102

Query Match 95.1%; Score 1163.8; DB 16; Length 1191;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 1171; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
Qy 1 ATGGAGCCCAACTCTCAAGAAACACCAAGTGTTCATGAAATGAAGATGTCAACTTT 60
Db 1 ATGGAGCCCAACTCTCAAGAAACACCAAGTGTTCATGAAATGAAGATGTCAACTTT 60
Qy 61 GACCACTTTGAAATTTTCCGAGCCATTTGGGAAAGGCGAGTTTGGGAGGCTCTGATTTGA 120
Db 61 GACCACTTTGAAATTTTCCGAGCCATTTGGGAAAGGCGAGTTTGGGAGGCTCTGATTTGA 120
Qy 121 CAGAAGAATGATACCAAGAAGATGTACGCAATGAAGTACATGAATAAACAAGTGGGTG 180
Db 121 CAGAAGAATGATACCAAGAAGATGTACGCAATGAAGTACATGAATAAACAAGTGGGTG 180
Qy 181 GAGCGCAATGAAGTGAAGAAATGTCTTCAAGAACTCCAGATCATGCGAGGTCTCGAGCAC 240
Db 181 GAGCGCAATGAAGTGAAGAAATGTCTTCAAGAACTCCAGATCATGCGAGGTCTCGAGCAC 240
Qy 241 CCTTCTCTGTTAAATTTTGTGTTATTCCTTCCAGATGAGGAAGACATGTTTCATGTTG 300
Db 241 CCTTCTCTGTTAAATTTTGTGTTATTCCTTCCAGATGAGGAAGACATGTTTCATGTTG 300
Qy 301 GACCTCTCTGTTGGTGGAGACCTGCGTTATCACCTGCAACAGAACGCTCCACTTCAAGGAA 360
Db 301 GACCTCTCTGTTGGTGGAGACCTGCGTTATCACCTGCAACAGAACGCTCCACTTCAAGGAA 360
Qy 361 GAAACAGTGAAGCTCTTTCATCTGTGAGCTGGTATGCGCCCTGGACTACCTCGAGAACCG 420
Db 361 GAAACAGTGAAGCTCTTTCATCTGTGAGCTGGTATGCGCCCTGGACTACCTCGAGAACCG 420
Qy 421 CGCATCATTCACAGGATATGAAGCTTGACATATTTTACTTGTGACGACATGCGGACGCTG 480
Db 421 CGCATCATTCACAGGATATGAAGCTTGACATATTTTACTTGTGACGACATGCGGACGCTG 480
Qy 481 CACATCAGATTTTCAACATTTGTCGATGCTGCCAGGAGACACAGATATACCAACCATG 540
Db 481 CACATCAGATTTTCAACATTTGTCGATGCTGCCAGGAGACACAGATATACCAACCATG 540
Qy 541 GCTGGCACCAAGCCTTACATGGCACCTGAGATGTTTCAGTCTCCAGAAAGGAGGAGCTAT 600
Db 541 GCTGGCACCAAGCCTTACATGGCACCTGAGATGTTTCAGTCTCCAGAAAGGAGGAGCTAT 600
Qy 601 TCCCTTCTGTTGATCTGCTGGTGGTCCCTGGAGTGAAGGATATGAATGCTGAGAGGCGG 660
Db 601 TCCCTTCTGTTGATCTGCTGGTGGTCCCTGGAGTGAAGGATATGAATGCTGAGAGGCGG 660
Qy 661 AGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAAATTTGTACACACCTTTGAGACG 720
Db 661 AGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAAATTTGTACACACCTTTGAGACG 720
Qy 721 ACTGTTGTAACTTACCTTCTGCTGGTCAAGGAAATGTTGTCATCTTTTAAAGGCTA 780
Db 721 ACTGTTGTAACTTACCTTCTGCTGGTCAAGGAAATGTTGTCATCTTTTAAAGGCTA 780
Qy 781 CTCGAACTTAATCAGACCAACGATTTTCTCAGTTATCTGATGTCGAGAACTTCCCGTAT 840
Db 781 CTCGAACTTAATCAGACCAACGATTTTCTCAGTTATCTGATGTCGAGAACTTCCCGTAT 840
Qy 841 ATGAATGATATAAACTGGGATGCGAGTTTTCAGAAAGGAGGCTCATTTCCAGGTTTCATCT 900
Db 841 ATGAATGATATAAACTGGGATGCGAGTTTTCAGAAAGGAGGCTCATTTCCAGGTTTCATCT 900
Qy 901 AATAAAGCGAGCTGAATTTGTGATCTTACCTTTCAGAAAGGAAATGATTTTGGAGTCC 960
Db 901 AATAAAGCGAGCTGAATTTGTGATCTTACCTTTCAGAAAGGAAATGATTTTGGAGTCC 960
Qy 961 AAACCTCTACATAAGAAAAAAGCGTCTGCAAGAGGAGGAGGATATGAGGAATGC 1020
Db 961 AAACCTCTACATAAGAAAAAAGCGTCTGCAAGAGGAGGAGGATATGAGGAATGC 1020
Qy 1021 GATTCCTCTCAGACATGCTCTCTTCAAGAGACACCTTGAATGCTGCTCCAGAGGAGTTCCATA 1080

Db 1021 GATTCTCTCAGACATGCTCTTCTCAAGAGCACCTTGACTCTGTCCAGAAAGGAGTTTCATA 1080
Qy 1081 ATTTTCAACAGAGAAAGTAAACAGGAGCTTTTAAACAAAGACAAACCAATCTAGCCTTG 1140
Db 1081 ATTTTCAACAGAGAAAGTAAACAGGAGCTTTTAAACAAAGACAAACCAATCTAGCCTTG 1140
Qy 1141 GAACAAACCAAGACCCCAAGTGCACAAATGGACAAATGGACA 1183
Db 1141 GAACAAACCAAGACCCCAAGTGCACAAATGGACAAATGGACA 1183

RESULT 11

US-10-410-764-100
; Sequence 100, Application US/10410764
; Publication No. US20040005664A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Meyers, Rachel E.
; APPLICANT: MacBeth, Kyle J.
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Rudolph-Owen, Laura A.
; APPLICANT: Weich, Nadine S.
; APPLICANT: Olandt, Peter J.
; APPLICANT: Tsai, Fong-Ying
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Carroll, Joseph M.
; TITLE OF INVENTION: 26199, 33530, 33949, 47148, 50226,
; TITLE OF INVENTION: 58764, 62113, 32144, 32235, 23565, 13305, 14911, 86216,
; TITLE OF INVENTION: 25206 AND 8843 MOLECULES AND USES THEREFOR
; FILE REFERENCE: MPI03-0520NMN
; CURRENT APPLICATION NUMBER: US/10/410,764
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: US 09/924,358
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/229,300
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: US 10/350,553
; PRIOR FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: US 60/351,572
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: US 09/966,614
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US 60/238,054
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: US 10/281,094
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US 60/347,815
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 10/076,535
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US 60/269,440
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 100
; LENGTH: 1281
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (49)...(1239)
US-10-410-764-100

Query Match 95.1%; Score 1163.8; DB 16; Length 1281;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 1171; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
Qy 1 ATGGAGGCAACACTTCAAGAAAACCCAGAGTGTGATGAATGAAGATGCAACTTT 60
Db 49 ATGGAGGCAACACTTCAAGAAAACCCAGAGTGTGATGAATGAAGATGCAACTTT 108

Qy 61 GACCCTTTGAAATTTTTCGAGCCATTGGGAAAGCGAGTTTTTGGAAAGGTCTGCAATTGTA 120
Db 109 GACCCTTTGAAATTTTTCGAGCCATTGGGAAAGCGAGTTTTTGGAAAGGTCTGCAATTGTA 168
Qy 121 CAGAAGATGATACCAAGAGATGTAGCAATGAAGTACATGAATAACAAGTGGGTG 180
Db 169 CAGAAGATGATACCAAGAGATGTAGCAATGAAGTACATGAATAACAAGTGGGTG 228
Qy 181 GAGGCAATGAAGTGAAGATGTCTTCAAGGAACCTCCAGATCATGCGAGGTCTCGAGCAC 240
Db 229 GAGGCAATGAAGTGAAGATGTCTTCAAGGAACCTCCAGATCATGCGAGGTCTCGAGCAC 288
Qy 241 CCTTTCTCGTTAATTTTGTGGTATTCCTTCAAGATGAGGAAGACATGTTTCATGTTG 300
Db 289 CCTTTCTCGTTAATTTTGTGGTATTCCTTCAAGATGAGGAAGACATGTTTCATGTTG 348
Qy 301 GACCTCTCTGGGTGAGACCTGCGTTATCACCTGCAACAGACGTCCTCACTTCAAGGA 360
Db 349 GACCTCTCTGGGTGAGACCTGCGTTATCACCTGCAACAGACGTCCTCACTTCAAGGA 408
Qy 361 GAAACAGTGAAGCTCTTTCATCTGTGAGCTGGTCAATGGCCCTGGACTACCTGCAGAAC 420
Db 409 GAAACAGTGAAGCTCTTTCATCTGTGAGCTGGTCAATGGCCCTGGACTACCTGCAGAAC 468
Qy 421 CGCATCATTCACAGGGATATGAAGCCTGACAATAATTTTACTTGACGAACATGGGCACGTG 480
Db 469 CGCATCATTCACAGGGATATGAAGCCTGACAATAATTTTACTTGACGAACATGGGCACGTG 528
Qy 481 CACATCAGATTTCAACATTTGCTGCGATGCTGCGCCAGGAGGACACAGATTTACCACATG 540
Db 529 CACATCAGATTTCAACATTTGCTGCGATGCTGCGCCAGGAGGACACAGATTTACCACATG 588
Qy 541 GCTGGCACCAAGCCTTACATGGCACCTGAGATGTTTCAAGTCCAGAAAAGGACAGGCTAT 600
Db 589 GCTGGCACCAAGCCTTACATGGCACCTGAGATGTTTCAAGTCCAGAAAAGGACAGGCTAT 648
Qy 601 TCCTTTGCTGTTGACTGCTGGTCCCTGGAGTGCAGCATATGAATCTGTGAGAGGCCG 660
Db 649 TCCTTTGCTGTTGACTGCTGGTCCCTGGAGTGCAGCATATGAATCTGTGAGAGGCCG 708
Qy 661 AGACCGTATCATATTCGCTCCAGTACTTCCAGAAAGGAAATTTGACACAGCTTTGACACG 720
Db 709 AGACCGTATCATATTCGCTCCAGTACTTCCAGAAAGGAAATTTGACACAGCTTTGACACG 768
Qy 721 ACTGTTGTAATTTACCCCTTCTGCTGCTGTCACAGAAATGGTGTGCTCTTTAAAAAGCTA 780
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Db 1129 ATTTTCAACAGAGAAAAAGTAAACAGGAGCTTTTAAACAAAAAGACAAACCAATCTAGCCTTG 1188
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Db 1189 GAACAAACCAAGACCCACAAAGGTGAGGATGGTCAGATAACA 1231
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; Sequence 1, Application US/09801876B
; Patent No. US20020127683A1
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001160
; CURRENT APPLICATION NUMBER: US/09/801.876B
; CURRENT FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1485
; TYPE: DNA
; ORGANISM: Human
US-09-801-876B-1
Query Match 94.8%; Score 1160.6; DB 9; Length 1485;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 1169; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
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Db 3 ATGGGAGCCAACTTCAAGAAAACCCACGAGTGTGATGAAATGAAGATGTCAACTTT 62
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Qy 301 GACCTCTGCTGGTGGAGACCTGGTTATCACCTGCAACAGACGTCCTCAAGGAA 360
Db 303 GACCTCTGCTGGTGGAGACCTGGTTATCACCTGCAACAGACGTCCTCAAGGAA 362
Qy 361 GAAACAGTGAAGCTTTCATCTGTGAGCTGCTGATGCGCCCTGGACTACCTCGAAGACCA 420
Db 363 GAAACAGTGAAGCTTTCATCTGTGAGCTGCTGATGCGCCCTGGACTACCTCGAAGACCA 422
Qy 421 CGCATATTCACAGGATATGAAGCTGACAAATATTTTACTTGAACGACATGCGGACCGTG 480
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Qy 1081 ATTTTCAACAGAGAAAAGTAAACAGGGACTTTTAAACAAAAGACAAACCAAAATCTAGCCTTG 1140
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Db 1143 GAACAAACCAAGACCCACCAAGGTGAGGTGGTCAGAAATAACA 1185
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; Sequence 1, Application US/10254869
; Publication No. US20030027307A1
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001160DIV
; CURRENT APPLICATION NUMBER: US/10/254.869
; CURRENT FILING DATE: 2002-09-26
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1485
; TYPE: DNA
; ORGANISM: Human
US-10-254-869-1

Query Match 94.8%; Score 1160.6; DB 14; Length 1485;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 1169; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
Qy 1 ATGGGAGCCAACTTCAAGAAAACCCACGAGTGTGATGAAATGAAGATGTCAACTTT 60
Db 3 ATGGGAGCCAACTTCAAGAAAACCCACGAGTGTGATGAAATGAAGATGTCAACTTT 62
Qy 61 GACCACCTTGAATTTTGGCGAGCCATTTGGGAAAGCGAGTTTGGGAGGTCTGCATTTGA 120
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Qy 121 CAGAGAAATGATACCAAGAAAGTGTACGCAATGAAGTACATGAATAAACAAGAGTGGTG 180
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Qy 361 GAAACAGTGAAGCTCTTCATCTGTGAGCTGGTTCATGGCCCTGGATCTCTGAGAACCA 420
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Db 603 TCTTTTGTCTGTTGACTGTTGTTGCTGGAGTGGCGATATGACTCTGAGAGGCCGG 662
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Qy 721 ACTGTTGTAACTTACCTTCTGCTGTTCAAGGAAATGGTGTCACTTCTTAAAGGCTA 780
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Db 783 CTCGAACCTATTCACAGACCAAGATTTTCTCAGATTTATCTGATGTCAGAACTTCCCGTAT 842
Qy 841 ATGAATGATATAAATCGGATGAGTCTTTTTCAGAGAGGCTCAITTCAGGTTTCAATTCCT 900
Db 843 ATGAATGATATAAATCGGATGAGTCTTTTTCAGAGAGGCTCAITTCAGGTTTCAATTCCT 902
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US-10-667-442-1

; Sequence 1, Application US/10667442

; Publication No. US20040043466A1

; GENERAL INFORMATION:

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; APPLICANT: YE, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001160DIV II
; CURRENT APPLICATION NUMBER: US/10/667,442
; CURRENT FILING DATE: 2003-09-23
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1485
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-667-442-1
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Query Match 94.8%; Score 1160.6; DB 16; Length 1485;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 1169; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 1 ATGGGAGCCAACTTCAAGAAAACCAACCAAGTGTTCATGAAAATGAAGATGTCAACTTT 60
Db 3 ATGGGAGCCAACTTCAAGAAAACCAACCAAGTGTTCATGAAAATGAAGATGTCAACTTT 62
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Qy 661 AGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAAATTTGTACACACGTTTGAGACG 720
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Db 783 CTCGAACCTAATCCAGACCACGAGTTTCTCAGTTATCTGATGTCCAGAACTTCCCGTAT 842
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Qy 1081 ATTTTCAACAGAGAAAAAGTAAACAGGGACTTTTAAACAAAAGACAAACCAAAATCTAGCCTTG 1140
Db 1083 ATTTTCAACAGAGAAAAAGTAAACAGGGACTTTTAAACAAAAGACAAACCAAAATCTAGCCTTG 1142
Qy 1141 GAACAAACCAAGACCCACCAAGTGACAAATGGACAAATGGACA 1183
Db 1143 GAACAAACCAAGACCCACCAAGTGAGGATGGTCCAGAAATACA 1185

RESULT 15
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; Sequence 231, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1e1 full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 231
; LENGTH: 2063
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-108-260A-231

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Best Local Similarity 99.7%; Pred. No. 3.3e-301;
Matches 1034; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 394 GACCACCTTGAATTTTGGCGGACATTTGGGAAAGGCGAGTTTGGGAGGCTCGCATTTGA 453
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Db 754 CGCATCATTTCAACAGGATATGAAGCCCTGACAATATTTTACTTGACGAAACATGGGCACGTG 813
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Db 814 CACATCACAGATTTCAACATTTGCTGCGATGCTGCCCGGAGAGACACAGATATACCACCATG 873
Qy 541 GCTGGCACCAAGCTTTTACATGGCACCTTGAGATGTTTCCAGCTCCAGAAAAGGAGCAGGCTAT 600
Db 874 GCTGGCACCAAGCTTTTACATGGCACCTTGAGATGTTTCCAGCTCCAGAAAAGGAGCAGGCTAT 933
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Db 934 TCCTTTGCTGTGACTGCTGGTGGTCCCTGGGAGTGACGCGCATATGAACCTGCTGAGAGGCCGG 993
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Db 994 AGACCGTATCATATTTGCTCCAGTACTTCCAGCAAGGAAATTTGTACACAGCTTTTGAGACG 1053
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Db 1054 ACTGTTGTAACCTTACCCCTTCTGCTGTCACAGGAAATGCTGTCACCTTCTTAAAAAGCTA 1113
Qy 781 CTCGAAACCTAATCCAGACCAACGATTTTCTCAGTTATCTGATGTCCAGAACTTCCCGTAT 840
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Qy 841 ATGAATGATATAAAGTGGGATGAGTTTTCAGAAAGGCTCATTCAGGTTTTCATTCCT 900
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GenCore version 5.1.6
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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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6	661	54.0	711	4	US-09-841-683-6
7	660	53.9	678	4	US-09-841-683-4
8	484.8	39.6	1257	4	US-09-799-875-15
9	484.8	39.6	1257	4	US-09-799-875-13
10	470	38.4	1864	4	US-09-819-607-1
11	181.8	14.9	148567	4	US-09-801-876B-3
12	181.8	14.9	148567	4	US-10-254-869-3
13	134.2	11.0	1008	4	US-09-394-455-3
14	134.2	11.0	2549	3	US-09-467-082-3
15	134.2	11.0	2549	4	US-09-394-455-5
16	134.2	11.0	2608	4	US-09-394-455-35
17	134	10.9	819	4	US-09-270-767-1482
18	134	10.9	819	4	US-09-270-767-16764
19	133.6	10.9	1619	4	US-09-394-455-14
20	122.6	10.0	25603	4	US-09-819-607-3
21	121.4	9.9	1788	4	US-09-417-197-68
22	121.4	9.9	2211	4	US-09-394-455-39
23	120.4	9.8	1498	3	US-09-509-902A-6
24	120.4	9.8	1961	3	US-09-509-902A-15
25	120.4	9.8	2204	1	US-08-221-817-12
26	120.4	9.8	2204	1	US-08-454-439-12
27	120.4	9.8	2204	5	PCT-US94-10487-12

28	120.4	9.8	2206	1	US-08-221-817-10	Sequence 10, Appl
29	120.4	9.8	2206	1	US-08-454-439-10	Sequence 10, Appl
30	120.4	9.8	2206	5	PCT-US94-10487-10	Sequence 10, Appl
31	120.4	9.8	2848	3	US-08-464-954A-2	Sequence 2, Appl
32	120.4	9.8	5276	4	US-09-233-857-2	Sequence 2, Appl
33	113	9.2	1599	3	US-09-256-465-1	Sequence 1, Appl
34	113	9.2	1599	3	US-09-167-322-3	Sequence 3, Appl
35	113	9.2	1599	4	US-09-023-555-1004	Sequence 1004, Ap
36	110.8	9.1	1662	4	US-09-802-117-1	Sequence 1, Appl
37	110.8	9.1	2249	4	US-09-802-117-5	Sequence 5, Appl
38	110	9.0	2370	3	US-09-031-295-1	Sequence 1, Appl
39	110	9.0	4438	4	US-09-566-921-81	Sequence 81, Appl
40	109.8	8.9	2599	6	5266464-1	Patent No. 5266464
41	109.2	8.9	1662	3	US-09-738-894A-1	Sequence 1, Appl
42	109.2	8.9	1662	4	US-09-964-469-1	Sequence 1, Appl
43	108.8	8.7	2754	3	US-09-429-322-3	Sequence 3, Appl
44	106.8	8.7	2311	2	US-08-712-709-6	Sequence 6, Appl
45	106.8	8.7	2311	3	US-09-111-444-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1

US-09-841-683-8

; Sequence 8, Application US/09841683

; Patent No. 6617147

; GENERAL INFORMATION:

; APPLICANT: Hu, Yi

; APPLICANT: Nepomichy, Boris

; APPLICANT: Wang, Xiaoming

; APPLICANT: Donoho, Gregory

; APPLICANT: Scoville, John

; APPLICANT: Walke, D. Wade

; TITLE OF INVENTION: No. 6617147el Human Kinase Proteins and Polynucleotides Encoding

; FILE REFERENCE: LEX-0167-USA

; CURRENT APPLICATION NUMBER: US/09/841,683

; PRIOR FILING DATE: 2001-04-24

; PRIOR FILING DATE: 2000-04-25

; PRIOR FILING DATE: 2000-04-25

; PRIOR FILING DATE: 2000-05-01

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 8

; LENGTH: 1224

; TYPE: DNA

; ORGANISM: homo sapiens

; US-09-841-683-8

Query Match 100.0%; Score 1224; DB 4; Length 1224;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ATGGAGCCACACTTCAAGAAACCCACAGTGTTCATGAAATGAAGATGCAACTTT	60
Db	1	ATGGAGCCACACTTCAAGAAACCCACAGTGTTCATGAAATGAAGATGCAACTTT	60
Qy	61	GACCACTTGAATTTTGGAGCCATTGGGAAAGCCAGTTTGGAAAGTCTGCATTGTA	120
Db	61	GACCACTTGAATTTTGGAGCCATTGGGAAAGCCAGTTTGGAAAGTCTGCATTGTA	120
Qy	121	CAGAAGATGATCAACAAAGATGTCGCAATGAAGTACATGAATAAACAAGTGCCTG	180
Db	121	CAGAAGATGATCAACAAAGATGTCGCAATGAAGTACATGAATAAACAAGTGCCTG	180
Qy	181	GAGCGCAATGAGTGAGAAATGCTTCAAGAACTCCAGATCATGCAGGCTCGAGCAC	240
Db	181	GAGCGCAATGAGTGAGAAATGCTTCAAGAACTCCAGATCATGCAGGCTCGAGCAC	240
Qy	241	CTTTCTCGTGAATTTTGTGTATTCTTCCAAGATGAGGAAGACATGTTTCATGTTGTG	300
Db	241	CTTTCTCGTGAATTTTGTGTATTCTTCCAAGATGAGGAAGACATGTTTCATGTTGTG	300

APPLICANT: Wang, Xiaoming
APPLICANT: Donoho, Gregory
APPLICANT: Scoville, John
APPLICANT: Walke, D. Wade
TITLE OF INVENTION: No. 6617147el Human Kinase Proteins and Polynucleotides Encoding
FILE REFERENCE: LEX-0167-USA
CURRENT APPLICATION NUMBER: US/09/841,683
CURRENT FILING DATE: 2001-04-24
PRIOR APPLICATION NUMBER: US 60/199,499
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: US 60/201,227
PRIOR FILING DATE: 2000-05-01
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12
LENGTH: 1675
TYPE: DNA
ORGANISM: homo sapiens
US-09-841-683-12

Query Match 100.0%; Score 1224; DB 4; Length 1675;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGGAGCCAACTTCAAGAAACCCACGAGTGTGATGAAATGAAGATGTCAACTTT 60
DB 413 ATGGGAGCCAACTTCAAGAAACCCACGAGTGTGATGAAATGAAGATGTCAACTTT 472
QY 61 GACCACCTTTGAAATTTTGGAGCCATTTGGAAAGGAGTGTGGAAGGTCTGCAATTGA 120
DB 473 GACCACCTTTGAAATTTTGGAGCCATTTGGAAAGGAGTGTGGAAGGTCTGCAATTGA 532
QY 121 CAGAAGAATGATACCAAGAGATGTAGCAATGAAGTACATGAATGAACAAAGTCCGCG 180
DB 533 CAGAAGAATGATACCAAGAGATGTAGCAATGAAGTACATGAATGAACAAAGTCCGCG 592
QY 181 GAGCGCAATCAAGTGAAGATGTCTCAAGGAATCTCAGATCATGATGAGGATCTGGAGCAC 240
DB 593 GAGCGCAATCAAGTGAAGATGTCTCAAGGAATCTCAGATCATGATGAGGATCTGGAGCAC 652
QY 241 CCTTTCCTGGTAAATTTTGTGTTATCTTCAAGAGATGAGGAACATGTTTCATGGTGGTG 300
DB 653 CCTTTCCTGGTAAATTTTGTGTTATCTTCAAGAGATGAGGAACATGTTTCATGGTGGTG 712
QY 301 GACCTCTGCTGGTGGAGACCTTTCATCTGTGAGCTGTGATGAGGATCTGAGGATCTGAGGAG 360
DB 713 GACCTCTGCTGGTGGAGACCTTTCATCTGTGAGCTGTGATGAGGATCTGAGGATCTGAGGAG 772
QY 361 GAAACAGTGAAGCTTTCATCTGTGAGCTGTGATGAGGATCTGAGGATCTGAGGAG 420
DB 773 GAAACAGTGAAGCTTTCATCTGTGAGCTGTGATGAGGATCTGAGGATCTGAGGAG 832
QY 421 CGCATCATTCACAGGATATGAAGCTGTGATGAGGATCTGAGGATCTGAGGATCTGAGGAG 480
DB 833 CGCATCATTCACAGGATATGAAGCTGTGATGAGGATCTGAGGATCTGAGGATCTGAGGAG 892
QY 481 CACATCAAGATTTCAACATTTGCGATGCTGCGGAGGAGACACAGATTTACCAATG 540
DB 893 CACATCAAGATTTCAACATTTGCGATGCTGCGGAGGAGACACAGATTTACCAATG 952
QY 541 GCTGCAACCAAGCTTTCATGAGGATGAGGATCTGAGGATCTGAGGATCTGAGGAG 600
DB 953 GCTGCAACCAAGCTTTCATGAGGATGAGGATCTGAGGATCTGAGGATCTGAGGAG 1012
QY 601 TCCTTTGCTGTGATGAGGATGAGGATCTGAGGATCTGAGGATCTGAGGAG 660
DB 1013 TCCTTTGCTGTGATGAGGATGAGGATCTGAGGATCTGAGGATCTGAGGAG 1072
QY 661 AGACCGTATCATATTTGCTGCTCAGTACTTCCAGCAAGGAAATTTGACACATTTGAGACG 720
DB 1073 AGACCGTATCATATTTGCTGCTCAGTACTTCCAGCAAGGAAATTTGACACATTTGAGACG 1132
QY 721 ACTGTTGTAACCTTACCCCTTCTGCTGGTGTGATGAGGATGAGGATCTGAGGATCTGAGGAT 780

QY 301 GACCTCTGCTGGTGGAGACCTGCTGTTATCACTGCAACAGAACGTCCTCAAGGAA 360
DB 301 GACCTCTGCTGGTGGAGACCTGCTGTTATCACTGCAACAGAACGTCCTCAAGGAA 360
QY 361 GAAACAGTGAAGCTTTCATCTGTGAGCTGTGATGAGGATCTGAGGATCTGAGGAG 420
DB 361 GAAACAGTGAAGCTTTCATCTGTGAGCTGTGATGAGGATCTGAGGATCTGAGGAG 420
QY 421 CGCATCATTCACAGGATATGAAGCTGTGATGAGGATCTGAGGATCTGAGGAG 480
DB 421 CGCATCATTCACAGGATATGAAGCTGTGATGAGGATCTGAGGATCTGAGGAG 480
QY 481 CACATCAAGATTTCAACATTTGCGATGCTGCGGAGGAGACACAGATTTACCAATG 540
DB 481 CACATCAAGATTTCAACATTTGCGATGCTGCGGAGGAGACACAGATTTACCAATG 540
QY 541 GCTGCAACCAAGCTTTCATGAGGATGAGGATCTGAGGATCTGAGGATCTGAGGAG 600
DB 541 GCTGCAACCAAGCTTTCATGAGGATGAGGATCTGAGGATCTGAGGATCTGAGGAG 600
QY 601 TCCTTTGCTGTGATGAGGATGAGGATCTGAGGATCTGAGGATCTGAGGAG 660
DB 601 TCCTTTGCTGTGATGAGGATGAGGATCTGAGGATCTGAGGATCTGAGGAG 660
QY 661 AGACCGTATCATATTTGCTGCTCAGTACTTCCAGCAAGGAAATTTGACACATTTGAGACG 720
DB 661 AGACCGTATCATATTTGCTGCTCAGTACTTCCAGCAAGGAAATTTGACACATTTGAGACG 720
QY 721 ACTGTTGTAACCTTACCCCTTCTGCTGGTGTGATGAGGATGAGGATCTGAGGATCTGAGGAT 780
DB 721 ACTGTTGTAACCTTACCCCTTCTGCTGGTGTGATGAGGATGAGGATCTGAGGATCTGAGGAT 780
QY 781 CTGCAACCTTAATCCAGCAACAGATTTCTGATGATGATGATGATGATGATGATGATGAT 840
DB 781 CTGCAACCTTAATCCAGCAACAGATTTCTGATGATGATGATGATGATGATGATGATGAT 840
QY 841 ATGAATGATATAAATGAGGATGAGGATTTTCAAGAGGATCTCAATCCAGGATTTCAATTCCT 900
DB 841 ATGAATGATATAAATGAGGATGAGGATTTTCAAGAGGATCTCAATCCAGGATTTCAATTCCT 900
QY 901 AATAAAGGAGGCTGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
DB 901 AATAAAGGAGGCTGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
QY 961 AATACCTTACATGAAGAAAGGCTGCTGCAAGAGGAGGATGAGGAAATGC 1020
DB 961 AATACCTTACATGAAGAAAGGCTGCTGCAAGAGGAGGATGAGGAAATGC 1020
QY 1021 GATTTCTTCTCAGACATGCTTCTTCAAGAGGATCTGATGATGATGATGATGATGATGATGAT 1080
DB 1021 GATTTCTTCTCAGACATGCTTCTTCAAGAGGATCTGATGATGATGATGATGATGATGATGAT 1080
QY 1081 ATTTTCAACAGAGAAAGTAAACAGGATTTTAAACAGAGGATTTTAAACAGAGGATTTTAAAC 1140
DB 1081 ATTTTCAACAGAGAAAGTAAACAGGATTTTAAACAGAGGATTTTAAACAGAGGATTTTAAAC 1140
QY 1141 GAAACACCAAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGAT 1200
DB 1141 GAAACACCAAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGAT 1200
QY 1201 TTTTCAGACCTCGAAAGTTTCATAA 1224
DB 1201 TTTTCAGACCTCGAAAGTTTCATAA 1224

RESULT 2
US-09-841-683-12
; Sequence 12, Application US/09841683
; Patent No. 6617147
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Nepomnichy, Boris

	Query Match	95.2%	Score 1165.4	DB 4	Length 1191
	Best Local Similarity	99.1%	pred. No. 0		
	Matches 1172	Conservative 0	Mismatches 11	Indels 0	Gaps 0
Qy	1	ATGGGAGCCACACTTCAGGAAACCCAGCGTGTTCATGAGAAATGAAGATGCAACTTT	60		
Db	1	ATGGGAGCCACACTTCAGGAAACCCAGCGTGTTCATGAGAAATGAAGATGCAACTTT	60		
Qy	61	GACCACTTTGAAATTTTCGGAGCCATTGGGAAAGGCAGTTTTCGGAAAGGCTTCGATTGTA	120		

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RESULT 4
US-09-801-876B-1
; Sequence 1, Application US/09801876B
; Patent No.: 6492155
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001160
; CURRENT APPLICATION NUMBER: US/09/801,876B
; CURRENT FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1485
; TYPE: DNA
; ORGANISM: Human
US-09-801-876B-1

Query Match      94.8%; Score 1160.6; DB 4; Length 1485;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 1169; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY      1  ATGGAGGCAACACCTTCAAGAAACCCACGAGTGTGATGAATAAGAGATGTCAACTTT 60
DB      3  ATGGAGGCAACACTTCAAGAAACCCACGAGTGTGATGAATAAGAGATGTCAACTTT 62
QY      61  GACCACTTTGAAATTTTGGAGGCAATTTGGGAAAGGCTTTTGGGAAAGTGTCAATGTA 120
DB      63  GACCACTTTGAAATTTTGGAGGCAATTTGGGAAAGGCTTTTGGGAAAGTGTCAATGTA 122
QY      121  CAGAGAAATGATACCAAGAGATGTAGCAATGAAGTACATGAATAAACAAGTGGTG 180
DB      123  CAGAGAAATGATACCAAGAGATGTAGCAATGAAGTACATGAATAAACAAGTGGTG 182
QY      181  GAGCGCAATGAAGTGAAGAAATGTCTTCAAGGAATCTCAGATCATCGAGGCTCTGAGCAC 240
DB      183  GAGCGCAATGAAGTGAAGAAATGTCTTCAAGGAATCTCAGATCATCGAGGCTCTGAGCAC 242

US-10-254-869-1
; Sequence 1, Application US/10254869
; Patent No.: 6653117
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001160DIV
; CURRENT APPLICATION NUMBER: US/10/254,869
; CURRENT FILING DATE: 2002-09-26
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1485
; TYPE: DNA
; ORGANISM: Human
US-10-254-869-1

Query Match      94.8%; Score 1160.6; DB 4; Length 1485;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 1169; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY      1  ATGGAGGCAACACTTCAAGAAACCCACGAGTGTGATGAATAAGAGATGTCAACTTT 60
DB      3  ATGGAGGCAACACTTCAAGAAACCCACGAGTGTGATGAATAAGAGATGTCAACTTT 62
QY      61  GACCACTTTGAAATTTTGGAGGCAATTTGGGAAAGGCTTTTGGGAAAGTGTCAATGTA 120
DB      63  GACCACTTTGAAATTTTGGAGGCAATTTGGGAAAGGCTTTTGGGAAAGTGTCAATGTA 122
QY      121  CAGAGAAATGATACCAAGAGATGTAGCAATGAAGTACATGAATAAACAAGTGGTG 180
DB      123  CAGAGAAATGATACCAAGAGATGTAGCAATGAAGTACATGAATAAACAAGTGGTG 182
QY      181  GAGCGCAATGAAGTGAAGAAATGTCTTCAAGGAATCTCAGATCATCGAGGCTCTGAGCAC 240
DB      183  GAGCGCAATGAAGTGAAGAAATGTCTTCAAGGAATCTCAGATCATCGAGGCTCTGAGCAC 242
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QY      721  ACTGTTGTAACCTTACCTTCTGCTGTGTCAAGAAATGGTGTCACTTCTTAAAAAGCTA 780
DB      723  ACTGTTGTAACCTTACCTTCTGCTGTGTCAAGAAATGGTGTCACTTCTTAAAAAGCTA 782
QY      781  CTCGAACCTAATCCAGACCAACGATTTTCTCAGTTATCTGATGTCCAGAACTTCCCGTAT 840
DB      783  CTCGAACCTAATCCAGACCAACGATTTTCTCAGTTATCTGATGTCCAGAACTTCCCGTAT 842
QY      841  ATGAATCATATAAACTGGGATGCAGTTTTCAGAAAGAGGCTCATTCAGAGTTTCATTCCT 900
DB      843  ATGAATCATATAAACTGGGATGCAGTTTTCAGAAAGAGGCTCATTCAGAGTTTCATTCCT 902
QY      901  AATAAGGCGAGGCTGAATTTGTGATCTTACCTTTGAACTTTGAGGAAATGATTTTGAGTCC 960
DB      903  AATAAGGCGAGGCTGAATTTGTGATCTTACCTTTGAACTTTGAGGAAATGATTTTGAGTCC 962
QY      961  AAACCTCTACATAAGAAAAAAGGCTCTGGCAAGAGGAGGAGGATATGAGGAAATGC 1020
DB      963  AAACCTCTACATAAGAAAAAAGGCTCTGGCAAGAGGAGGAGGATATGAGGAAATGC 1022
QY      1021  GATTCCTTCTCAGACATGTCTTCTCAAGAGCACCTTGCATCTGTCCAGAAAGGAGTTCATA 1080
DB      1023  GATTCCTTCTCAGACATGTCTTCTCAAGAGCACCTTGCATCTGTCCAGAAAGGAGTTCATA 1082
QY      1081  ATTTTCAACGAGAAAAAGTAAACAGGAGCTTTTAAACAAAGAACACCAAAATCTAGCCTTG 1140
DB      1083  ATTTTCAACGAGAAAAAGTAAACAGGAGCTTTTAAACAAAGAACACCAAAATCTAGCCTTG 1142
QY      1141  GAACAAACCAAGAACCCACCAAGTGACAAATGGACAAATGACA 1183
DB      1143  GAACAAACCAAGAACCCACCAAGTGAGGATGGTCAGAAATAACA 1185
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RESULT 5
US-10-254-869-1
; Sequence 1, Application US/10254869
; Patent No.: 6653117
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001160DIV
; CURRENT APPLICATION NUMBER: US/10/254,869
; CURRENT FILING DATE: 2002-09-26
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1485
; TYPE: DNA
; ORGANISM: Human
US-10-254-869-1

Query Match      94.8%; Score 1160.6; DB 4; Length 1485;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 1169; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY      1  ATGGAGGCAACACTTCAAGAAACCCACGAGTGTGATGAATAAGAGATGTCAACTTT 60
DB      3  ATGGAGGCAACACTTCAAGAAACCCACGAGTGTGATGAATAAGAGATGTCAACTTT 62
QY      61  GACCACTTTGAAATTTTGGAGGCAATTTGGGAAAGGCTTTTGGGAAAGTGTCAATGTA 120
DB      63  GACCACTTTGAAATTTTGGAGGCAATTTGGGAAAGGCTTTTGGGAAAGTGTCAATGTA 122
QY      121  CAGAGAAATGATACCAAGAGATGTAGCAATGAAGTACATGAATAAACAAGTGGTG 180
DB      123  CAGAGAAATGATACCAAGAGATGTAGCAATGAAGTACATGAATAAACAAGTGGTG 182
QY      181  GAGCGCAATGAAGTGAAGAAATGTCTTCAAGGAATCTCAGATCATCGAGGCTCTGAGCAC 240
DB      183  GAGCGCAATGAAGTGAAGAAATGTCTTCAAGGAATCTCAGATCATCGAGGCTCTGAGCAC 242
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RESULT 7
US-09-841-683-4
; Sequence 4, Application US/09841683
; Patent No. 6617147
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Nepomnichy, Boris
; APPLICANT: Wang, Xiaoming
; APPLICANT: Donoho, Gregory
; APPLICANT: Scoville, John
; APPLICANT: Walke, D. Wade
; TITLE OF INVENTION: No. 6617147el Human Kinase Proteins and Polynucleotides Encoding
; FILE REFERENCE: LEX-0167-USA
; CURRENT APPLICATION NUMBER: US/09/841,683
; CURRENT FILING DATE: 2001-04-24
; PRIOR FILING DATE: 2000-04-25
; PRIOR FILING DATE: 2000-04-25
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 678
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-841-683-4

Query Match      53.9%; Score 660; DB 4; Length 678;
Best Local Similarity 100.0%; Pred. No. 4e-206;
Matches 660; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGGAGCCACACCTTCAAGAAAACCCACGAGTTTGTATGAAAATGAAGATGTCAACTTT 60
DB 1 ATGGGAGCCACACCTTCAAGAAAACCCACGAGTTTGTATGAAAATGAAGATGTCAACTTT 60
QY 61 GACCACTTTGAAATTTTGGAGCCATTGGGAAGCCAGTTTGGGAAGGTCTGCATTGTA 120
DB 61 GACCACTTTGAAATTTTGGAGCCATTGGGAAGCCAGTTTGGGAAGGTCTGCATTGTA 120
QY 121 CAGAGAATGATACCAAGAAGATGTACGCAATGAAGTATCATGAATAAACAAGTGCCTG 180
DB 121 CAGAGAATGATACCAAGAAGATGTACGCAATGAAGTATCATGAATAAACAAGTGCCTG 180
QY 181 GAGCGAATGAAGTGAAGATCTCTCAAGAACTCCAGATCATGCGAGGTCTGAGCAC 240
DB 181 GAGCGAATGAAGTGAAGATCTCTCAAGAACTCCAGATCATGCGAGGTCTGAGCAC 240
QY 241 CCTTTCTGTTAAATTTGTGGTATTTCTTCCAGATGAGGAAGACATGTTTCAATGTTGTG 300
DB 241 CCTTTCTGTTAAATTTGTGGTATTTCTTCCAGATGAGGAAGACATGTTTCAATGTTGTG 300
QY 301 GACCTCTGCTGGGTGGAGACCTGGTTTATCACTTCAAGCAAGACGTCCACTTCAAGGAA 360
DB 301 GACCTCTGCTGGGTGGAGACCTGGTTTATCACTTCAAGCAAGACGTCCACTTCAAGGAA 360
QY 361 GAAACAGTGAAGCTCTTCACTGTGAGCTGTGTCAGCCCTGAGTACCTTCAGAACAG 420
DB 361 GAAACAGTGAAGCTCTTCACTGTGAGCTGTGTCAGCCCTGAGTACCTTCAGAACAG 420
QY 421 CGCATATTCAGGGATATGAAGCTTGAATATTTTACTTGAAGCAATGAGGACAGTG 480
DB 421 CGCATATTCAGGGATATGAAGCTTGAATATTTTACTTGAAGCAATGAGGACAGTG 480
QY 481 CACATCAGATTTCAATGCTGCGATGCTGCGGAGGAGACACAGATTACCAACATG 540
DB 481 CACATCAGATTTCAATGCTGCGATGCTGCGGAGGAGACACAGATTACCAACATG 540
QY 541 GCTGSCACCAAGCCTTACATGGCACTTGAAGTGTTCAGTCCAGAAAAGGAGGAGGCTAT 600
DB 541 GCTGSCACCAAGCCTTACATGGCACTTGAAGTGTTCAGTCCAGAAAAGGAGGAGGCTAT 600
QY 601 TCCTTTGCTTTGATGTTGCTGCTGGAGTACGCGATATGAATCTGTCGAGAGGCCGG 660
DB 601 TCCTTTGCTTTGATGTTGCTGCTGGAGTACGCGATATGAATCTGTCGAGAGGCCGG 660
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Db 601 TCCTTTGCTTTGATGTTGCTGCTGGAGTACGCGATATGAATCTGTCGAGAGGCCGG 660

RESULT 8
US-09-799-875-15
; Sequence 15, Application US/09799875
; Patent No. 6638721
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Williamson, Mark
; TITLE OF INVENTION: No. 6638721el Human Protein Kinases and Uses
; FILE REFERENCE: 35800/209996
; CURRENT APPLICATION NUMBER: US/09/799,875
; CURRENT FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: 60/182,059
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 09/659,287
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-799-875-15
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Query Match      39.6%; Score 484.8; DB 4; Length 1257;
Best Local Similarity 66.7%; Pred. No. 2.2e-148;
Matches 728; Conservative 0; Mismatches 352; Indels 12; Gaps 2;

QY 28 CCAGTGTTCATGAAATGAAGATGTCACCTTTGACCACTTTGAAATTTTGGAGCAATT 87
DB 37 CCGTGTGTTTACCAACAGGAGGACGTGAACCTTCGACACTTCAGATCTCTTCGGGCATT 96
QY 88 GGGAAAGGCAAGTTTGGGAAGGTCTGCAATGTGACAGAAGATCATACCAAGAAGATGTAC 147
DB 97 GGGAAAGGCAAGTTTGGCAAGGTGTGCAATGTGCAAGAGCGGACACGAGAGATGTAC 156
QY 148 GCATGAAGTACATGAATATAAAGTGTGGAGCGCAATGAAGTGAAGATGTCTTC 207
DB 157 GCCATGAAGTACATGAATATAAAGTGTGGAGCGCAATGAAGTGAAGATGTCTTC 216
QY 208 AAGCAACTCCAGATCATGCAAGGTCTGGAGACCTTCTCTGTTTAAATTTGTTATTC 267
DB 217 CGGAGCTGGAGATCTTCAGAGGATCGAGCAGCTTCTCTGTTTAAATTTGTTATTC 276
QY 268 TTCAAGATGAGGAAGACATGTTTCAATGTTGTGGACCTCTCTGTTGTGGAGACCTGCGT 327
DB 277 TTCCAGAGCAGGAGGACATGTTTCAATGTTGTGGACCTCTCTGTTGTGGAGACCTGCGC 336
QY 328 TATCACTTCGACAGAACCTTCACTTCAAGGAAGAAACAGTGAAGCTTTCATCTGTAG 387
DB 337 TACCACTTCGACAGAACCTTCACTTCCGAGGACACGTTCTCCGAGGACACGTTGACATCTGCGAG 396
QY 388 CTGCTCATGCGCTGCACTACCTTCAGAACACGAGCGCATCTTCAAGGATATGAAGCCT 447
DB 397 ATGGCACTGGCTCTGCACTACCTTCGCGGCGACAGCATCATCCACAGATGTCAAGCT 456
QY 448 GACAAATTTTACTTGAAGAACATGGGACGTCGACATCAGAGTTTCAACATTTGCTGG 507
DB 457 GACAAATTTTCTCTGATGAGAGGACATGACACCTGACCGACTTCAACATTTGCGACC 516
QY 508 ATGCTGCCAGGAGACACAGATTACCACTTGGTGGCACCACCAAGCTTACATGCACT 567
DB 517 ATCATCAAGAGCAGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 576
QY 568 GAGATGTTTCAAGTCTC-----CAGAAAAGGAGCAGGCTATTTCTTTGCTGTTGACCTGG 621
DB 577 GAGATCTTCAACTCTTTTGTCAACCGGCGGACCGGCTACTCTCTTCGAGTGTGAGTGG 636
QY 622 TCCTTGGGAGTACGCGCATATGAATCTGTCGAGAGCGCGGACCGGTATCATATTCGTTCC 681
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Db 637 TCGTGGGGTGTATGGCTATAGCTGCTCGAGATGGAGGCCCTATGACATCCATCC 696
Qy 682 AGTACTTCCAGCAAGGAAATTTGTAACAACGTTTGAGACGACTGTTGTAACATTTACCTTTCT 741
Db 697 AGCAACGCGGTGGAGTCCCTGGTGCAGCTGTTTCAGCAACCGTGAGCGTCCAGTATGTCCCC 756
Qy 742 GCCTGGTTCACAGGAATGGTGTCACTTTCTTAAAGTACTACTCGAACCTTAATCCAGACCA 801
Db 757 ACGTGGTCCAGGAGATGGTGGCCCTTGTGCGAAGCTTCTCACTGTGAACCCCGAGAC 816
Qy 802 CGATTTTCTCAGTTATCTGATGTCCAGAACTTCCCGTATATGATATGATATAAACTGGGAT 861
Db 817 CGGTCTCCAGCTCCAGGAGCTGAGGACGCCCGCGCTGGCGGCTGCTGTGGAC 876
Qy 862 GCAGTTTTCAGAGAGGCTCAITTCAGGTTTCAATTCCTAATAAAGGAGGCTGAATGT 921
Db 877 CACCTGAGCGAGAGAGGTTGGAGCGCGGCTTCGTGCGCAACAAAGGCGCTGCACTGC 936
Qy 922 GATCCTACCTTTGAATTTGAGGAATGATTTTGGAGTCCAAACCTCTACATAAGAAAAA 981
Db 937 GACCCCACTTTGAGCTGGAGGAGATGATCTGGAGTCCAGGCCCTGCAAGAGAAAG 996
Qy 982 AAGCGTCTGGCAAGAGGA-----GAAGGATATAGGAAATCGGATTTCTTCAGACA 1035
Db 997 AAGGCTTGGCAAGAACAGTCCCGGGAACAAGCAGGAGCAGCTCCAGTCCGAGAT 1056
Qy 1036 TGTCTTCTCAAGAGCACCTTGACTCTGTGTCAGAGGAGTTTCAATTTTCAACAGAGAA 1095
Db 1057 GACTATCTCAAGACTGCTCGATGCCATCCAGCAAGACTTCGTGATTTTTTAAACAGAGAA 1116
Qy 1096 AAGTAAACAGG 1107
Db 1117 AAGCTGAAGAGG 1128
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RESULT 9

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US-09-799-875-13
; Sequence 13, Application US/09799875
; Patent No. 6638721
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Williamson, Mark
; TITLE OF INVENTION: No. 6638721el Human Protein Kinases and Uses
; TITLE OF INVENTION: Therefor
; FILE REFERENCE: 35800/209996
; CURRENT APPLICATION NUMBER: US/09/799,875
; CURRENT FILING DATE: 2001-03-06
; PRIOR FILING DATE: 2000-02-11
; PRIOR FILING DATE: 2000-02-11
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 1826
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (17)...(1273)
; US-09-799-875-13
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Query Match 39.6%; Score 484.8; DB 4; Length 1826;
Best Local Similarity 66.7%; Pred. No. 3e-148;
Matches 728; Conservative 0; Mismatches 352; Indels 12; Gaps 2;

Qy 28 CCACTGTTTGATGAAATGAAGATGTCAACTTTTGACCACTTTGAAATTTTCCGAGCCATT 87
Db 53 CCGGTGTTTGACGACAGGAGCGTGAATTCGACCACTTCAGATCTTCGGGCCATT 112
Qy 88 GGGAAAGGCAGTTTTGGAGGCTGTGCATTTGTACAGAAATGATACCAAGAAATGTAC 147
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RESULT 10

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Db 113 GGGAGGGCAGCTTTGGCAAGGTGTGCAATTTGTGAGAAAGCGGACACGGAGAAATGTAC 172
Qy 148 GCAATGAAGTACATGAATAAAACAAAGTGGTGGAGCGCAATGAAGTGAAGAAATGTCTTTC 207
Db 173 GCCATGAAGTACATGAATAAAACAAAGCAGCAGTGTGATCGAGCGCGCAGAGGTCCGCAAGCTCTTC 232
Qy 208 AAGGAACTCCAGATCATGCAAGGTCTGAGGACCCCTTCTCTGGTTAATTTTGTGTTATTC 267
Db 233 CGGAGCTGGAGATCTTCGAGGAGATCGAGACGCTTCTCTGGTGAACCTCTGGTACTTC 292
Qy 268 TTCCAAAGATGAGGAAGACATGTTTCATGTTGGTGACCTCTCTGGTGGTGGAGACCTTCGCT 327
Db 293 TTCCAGGACGAGGAGACATGTTTCATGTTGGTGACCTCTCTGGTGGGAGGAGCTTCGCGC 352
Qy 328 TATCACCCTGCAACAGAAAGCTCCACTTCAAGGAAGAAACAGTGAAGCTCTTCATCTGTGAG 387
Db 353 TACCACCCTGAGCAGAAAGCTGCAGTTCTCCGAGGACACGGGTGAGGCTGTACATCTGCGAG 412
Qy 388 CTGCTCATGGCCCTGGACTACCTGCAGAAACAGCGGCATCTTACACAGGATATCAAGCCT 447
Db 413 ATGGCACTGGCTCTGGACTACCTGCGCGGCAGACATCATCCACAGATGTCAAGCCT 472
Qy 448 GACAATATTTTACTTGAAGAACATGGGCAGCTGCACATCACAGATTTCAACATTTGCTGCG 507
Db 473 GACAACTTCTCTGGATGAGAGGACATGCAACCTGACCGACTTCAACATTTGCCACC 532
Qy 508 ATGCTGCCAGGAGACACAGATTTACCATGCTGGCACCAAGCTTTACATGGCACCT 567
Db 533 ATCATCAAGACGCGGAGCGGCGCATTTAGCAGGCACCAAGCCGTACATGGCTCCG 592
Qy 568 GAGATGTTCAAGTCTC-----CAGAAAGGAGCAGGCTATTTCTTGTGTTGACTGGTG 621
Db 593 GAGATCTTCCACTCTTTTGTCAACGCGGAGACCGGCTACTCTCTTCGAGGTGGATGGTG 652
Qy 622 TCCCTGGGAGTGACGCGCATATGAACCTGCTGAGAGCGGAGACCGCTATCATATTCGCTCC 681
Db 653 TCGTGGGGTGTATGGCTTATGAGCTGCTGGAGATGGAGGCCCTATGACATCCACTCC 712
Qy 682 AGTACTTCCAGCAAGGAAATTTGTAACAACGTTTGGACGACTGTTGTAACATTAACCTTCT 741
Db 713 AGCAACGCGTGGAGTCCCTGGTGCAGCTGTTTCAGCACCCGTGAGCGTCCAGTATGTCCCC 772
Qy 742 GCCTGGTTCACAGGAAATGGTGTCACTTTTAAAGCTACTCGAACCTTAATCCAGACCA 801
Db 773 ACCTGGTCCAAGGAGATGGTGGCTTCTGCGGAAAGCTCTCTACTGTGAACCCCGAGCAC 832
Qy 802 CGATTTTCTCAGTTTATCTGATGTCCAGAACTTCCCGTATATGATGATATAAACTGGGAT 861
Db 833 CGGTCTTCAGCTCCAGGACGTCAGGAGCCCGCGGCTGGCGGGGCTGCTGTGGAC 892
Qy 862 GCAGTTTTTTCAGAAAGGCTCATTTCCAGGTTTCAATTCCTAATAAAGGAGGCTGAATGT 921
Db 893 CACCTGAGCGAGAAAGAGGTTGGAGCGCGGCTTGTGCCCCAACAAAGGCGCTGCACTGC 952
Qy 922 GATCTACCTTTGAACTTGAGGAAATGATTTTGGAGTCCAAACCTCTACATAAGAAAAA 981
Db 953 GACCCCACTTTGAGCTGGAGGAGATGATCTCTGGAGTCCAGGCCCTGCAAGAAAGAG 1012
Qy 982 AAGCGTCTGCAAGAAAGGA-----GAAGGATATAGGAAATCGGATTTCTTCTCAGACA 1035
Db 1013 AAGCGTCTGGCCAAAGAAACAAGTCCCGGGAACAAGCAGGAGACAGCTCCAGTCCGAGAT 1072
Qy 1036 TGTCTTCTCAAGAGCACCTTGACTCTGTCCAGAGGAGTTTCAATTTTCAACAGAGAA 1095
Db 1073 GACTATCTTCAAGACTCGCTCGATGCCATCCAGCAAGACTTCGTGATTTTTTAAACAGAGAA 1132
Qy 1096 AAGTAAACAGG 1107
Db 1133 AAGCTGAAGAGG 1144
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US-09-819-607-1
; Sequence 1, Application US/09819607
; Patent No. 6686176
; GENERAL INFORMATION:
; APPLICANT: BEASLEY, Ellen et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; THEREOF
; FILE REFERENCE: CL001078
; CURRENT APPLICATION NUMBER: US/09/819,607
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1864
; TYPE: DNA
; ORGANISM: Human
US-09-819-607-1

Query Match 38.4%; Score 470; DB 4; Length 1864;
Best Local Similarity 66.1%; Pred. No. 2.2e-143;
Matches 715; Conservative 0; Mismatches 355; Indels 12; Gaps 2;

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QY 38 ATGAAATCAAGATGTCACCTTTGACCACTTTGAAATTTTGGAGCCATTGGGAAGCA 97
DB 89 AAGCAGAGAGCGATGAACTTCGACCACTTCAGATCCTTCGGGCCATTGGGAAGCA 148
QY 98 GTTTTGGGAAGTCTGCATTTGACAGAAATGATACCAAGAAAGATGTACGCAATGAAGT 157
DB 149 GCTTTGGCAAGTGTGATTTGTCAGAGCGGACACGAGAGATGTACGCCATGAAGT 208
QY 158 ACATGAAATCAAGAGTGTGAGCGGATGAAGTGAAGATGTCCTTCAAGGAATCC 217
DB 209 ACATGAAATCAAGAGTGTGAGCGGATGTGAGCGGATGTGAGCGGATGTGAGCGGATGTG 268
QY 218 AGATCATGAGGCTCTGAGGACCTTCTCTGTTAAATTTGTTGATTCCTTCAAGATG 277
DB 269 AGATCTGAGAGATGAGGACGCTTCTCTGTTAAATTTGTTGATTCCTTCAAGATG 328
QY 278 AGGAAGACATGTTCAATGTTGAGGACCTCTCTGTTGAGGACCTGTTTATCACCTGC 337
DB 329 AGGAGGACATGTTCAATGTTGAGGACCTCTCTGTTGAGGACCTGTTTATCACCTGC 388
QY 338 AACAGAGCTCCACTTCAAGNAGAAACAGTGAAGCTTCTATCTGTGAGCTGTGATGG 397
DB 389 AGCAGAGCTGTCAGTTCTCCGAGGACACGTTGAGGCTGTATCTGCGAGATGCGACTGG 448
QY 398 CCTCGACTTACCTGCAGAACACGCGCATCTTACAGGAGATGATGAAGCTGCACATATTT 457
DB 449 CTCTGACTTCTGCGGCGCAGCATCTTCCACAGAGATGTGAGCTGCACATATTT 508
QY 458 TACTTGACGAACATGGGCAAGTGCACATCAGAGATTTCAACATTTCTGCGATGCTGCCA 517
DB 509 TCCCTGATGAGAGGACATGCACACCTTACCGACTTCAACATTTGCCACCATCATCAAG 568
QY 518 GGGAGACACAGATTAACCACTGCTGAGCAGGACCTTACATGCGACCTGAGATGTCA 577
DB 569 ACGGGAGCGGCGGACGATTTAGCAGGACCAAGCCGATACATGGCTCCGAGATCTTCC 628
QY 578 GCTC-----CAGAAAGAGCAGGCTATTCTTGTGTTGTTGACTTGGTGTCTCGGAG 631
DB 629 ACTCTTTGTGTCACGCGGAGCCGCTACTCTTCTGAGGTGATGTGTTGTTGTTGGGG 688
QY 632 TGACGGCATATGAATCTGAGAGCGCGGACCGATATCATATTTGCTTCCAGTACTTCCA 691
DB 689 TGATGGCTATGAGTGTGAGGATGAGGCGCTATGACATCCATCCAGCAACGCCG 748
QY 692 GCAAGGAATTTGACACAGTTTGAAGCAGTGTGTAACCTTACCTTCTGCTGTTGCTAC 751
DB 749 TGAAGTCCCTGGTGCAGCTGTTTGAAGCAGTGTGTAACCTTACCTTCTGCTGTTGCTAC 808
QY 752 AGGAATGGTGTCACTTCTTAAAGAGCTTACTTCAACCTTAATCCAGACCAACGATTTTCTC 811
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DB 809 AGGAGATGGTGGCTTGTGCGGAAGTCTCTCACTGTGAACCCCGAGCACGGCTCTCCA 868
QY 812 AGTTATCTGATGTCAGAACTTCCGATATATGAATATAAATCGGATGCAGTTTTC 871
DB 869 CCCTCCAGAGCTGAGGAGCCCGGGCTGGCGGGCTGTGGGACCCACCTGAGCG 928
QY 872 AGAAGAGCTCATTTCCAGGTTTCAATCTTAATAAGGAGGCTGAATTTGTGATCCTACCT 931
DB 929 AGAAGAGGTTGGAGCCGGCTTCTGTCACCAAAAGCCGCTGCTCACTGCGACCCACCT 988
QY 932 TTGAAGTGAAGAAATGATTTTGGAGTCCAAACCTCTACATAAGAAAAAAGGCTGTGG 991
DB 989 TTGAGCTGGAGGAGATGATCTGAGTCCAGGCCCTGCAAGAGAAAGAGCGCTGG 1048
QY 992 CAAAGAAAGGA-----GAAGGATATGAGAAATCGGATTTCTCTCAGACATGTCTTCTTC 1045
DB 1049 CCAAGAACAGTCCCGGACCAACAGCAGGAGACAGTCCCGAGTCCGAGATGACTATCTTC 1108
QY 1046 AAGAGCAGCTTGTCTGTCCAGAGGAGTTCATAATTTTCAACAGAGAAAAAGTAAACA 1105
DB 1109 AAGACTGCTCGATGTCATCCAGCAAGACTTCGTGATTTTAAACAGAGAAAAAGCTGAAGA 1168
QY 1106 GG 1107
DB 1169 GG 1170
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RESULT 11
US-09-801-876B-3
; Sequence 3, Application US/09801876B
; Patent No. 6492155
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; THEREOF
; FILE REFERENCE: CL001160
; CURRENT APPLICATION NUMBER: US/09/801,876B
; CURRENT FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 148567
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(148567)
; OTHER INFORMATION: n = A, T, C or G
US-09-801-876B-3

Query Match 14.9%; Score 181.8; DB 4; Length 148567;
Best Local Similarity 89.9%; Pred. No. 2.8e-47;
Matches 195; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

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QY 252 TAATTTGTGATTTCTTCAAGATGAGGAAGACATGTTTCATGGTGGTGGACCTCTGCT 311
DB 86036 TAATTCAGGTATCTTCCAGATGAGGAAGACATGTTTCATGGTGGTGGACCTCTGCT 86095
QY 312 GGTGAGGACCTGCTGATTCACCTGCAACAGAGCTCCACTTCAAGAGAAACAGTGAA 371
DB 86096 GGTGAGGACCTGCTGATTCACCTGCAACAGAGCTCCACTTCAAGAGAAACAGTGAA 86155
QY 372 GCTCTTTCATCTGTGAGTGTGATGGCCCTGAGTACTACCTGCAAGAACAGCGCATATTTCA 431
DB 86156 GCTCTTTCATCTGTGAGTGTGATGGCCCTGAGTACTACCTGCAAGAACAGCGCATATTTCA 86215
QY 432 CAGGATATGAAGCCCTGACAAATATTTTACTTGACGAA 468
DB 86216 CAGGTCAAGTCCAGAGAGATGGCCATGAACGTA 86252
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RESULT 12

US-10-254-869-3
; Sequence 3, Application US/10254869
; Patent No. 6653117
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEROSF
; FILE REFERENCE: CLO01160DIV
; CURRENT APPLICATION NUMBER: US/10/254,869
; CURRENT FILING DATE: 2002-09-26
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 148567
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(148567)
; OTHER INFORMATION: n = A,T,C or G
US-10-254-869-3

Query Match 14.9%; Score 181.8; DB 4; Length 148567;
Best Local Similarity 89.9%; Pred. No. 2.8e-47;
Matches 195; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 252 TAAATTTGGTATTCTTCCAAAGATGAGGAAGACATGTTTCATGGTGGTGGACCTCCTGCT 311
DB 86036 TAAATCCAGGTATTCTTCCAAAGATGAGGAAGACATGTTTCATGGTGGTGGACCTCCTGCT 86095

QY 312 GGGTGGAGACCTCGCTTATCACCTGCAACAGAACGTCCTTCAAGGAAGAAAACAGTGAA 371
DB 86096 GGGTGGAGACCTCGCTTATCACCTGCAACAGAACGTCCTTCAAGGAAGAAAACAGTGAA 86155

QY 372 GCTCTTTCATCTGTGAGCTGGTCAATGCGCCCTGGACTACCTGCAGAACCCAGCGCATCTCA 431
DB 86156 GCTCTTTCATCTGTGAGCTGGTCAATGCGCCCTGGACTACCTGCAGAACCCAGCGCATCTCA 86215

QY 432 CAGGGATATGAAGCCTGACAAATATTTTACTTGCACGAA 468
DB 86216 CAGGTCACTCAAGTCCAGGAGATGCCATGAACGTA 86252

RESULT 13
US-09-394-455-3
; Sequence 3, Application US/09394455
; Patent No. 6531305
; GENERAL INFORMATION:
; APPLICANT: Witman, George F.
; APPLICANT: San Agustin, Jovenal
; APPLICANT: Leszyk, John D.
; TITLE OF INVENTION: SPERM ASSOCIATED PROTEIN KINASE POLYPEPTIDES, CORRESPONDING
; TITLE OF INVENTION: NUCLEIC ACIDS, AND METHODS OF USE
; FILE REFERENCE: 07917/078001
; CURRENT APPLICATION NUMBER: US/09/394,455
; CURRENT FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 60/099,771
; PRIOR FILING DATE: 1998-09-10
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1008
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1008)
US-09-394-455-3

Query Match 11.0%; Score 134.2; DB 4; Length 1008;
Best Local Similarity 54.3%; Pred. No. 2.6e-33;
Matches 324; Conservative 0; Mismatches 258; Indels 15; Gaps 2;

112 TGCATTGTTACAGAAAGATGATACCAAGAGAGATGTTCACCAATGAGTACATGATTAACA 171
Db 255 ATGCTGGTGAACAACAAGAGAGACCGGGAACCACTATGCCATGAAGATCCTCGACAACAG 314
Qy 172 AAGTGGTGGAGCGCAATCAAGTGAAGAAATGCTTTCAAGGAACTTCAGAGTATCATGCAAGGT 231
Db 315 AAGGTGGTGAACACTGAAACACAGATCGAACACACCCTGAATGAAAGCGCATCCTCGAAGCT 374
Qy 232 CTGGAGCACCTTTCTCTGGTTAAATTTGTGGTATTCCTTCCAAGTGAAGGAGACATGTTTC 291
Db 375 GTCAAACTTTCCGTTCTCTCGTCAAACTCGAGTTCTCTTCAAGGACAACCTCAAACTTTATAC 434
Qy 292 ATGTGGTGGAGCCTCCTCTGTGGTGGAGACCTCGGTTTATCACTGTGCACCAAGAACCTGCCAC 351
Db 435 ATGTGTCATGAGTACGTGCCCGCGGGAGATGTTCTCACACCTACGGCGGATCGGAAG 494
Qy 352 TTCAAGGAAGAAACAAGTGAAGCTCTTCAATCTGTAGCTGTGTCATGGCCCTGGACTACCTG 411
Db 495 TTCAAGTGAAGCCCAATGCCCGTTTCTACGCGGCCAGATCGTCTGCACTTTTGAGTATCTG 554
Qy 412 CAGAACCAAGCGCATCAATTCACAGGATATGAAGCTGCACAATATTTTACTTTGACGAACAT 471
Db 555 CACTCGCTGGATCTCATCTACAGGACCTGAAGCGGAGAACTGTCTCATTTGACCAAGAG 614
Qy 472 GGGCAGTGTGCATCACAGATTTCAACATGCTCGGATGCTGCCAGGAGAGACAGATT 531
Db 615 GGCTACATTCAGGTGACAGACTTCGGTTTCGCCAA-----GGCGGTGAAGGGCCGCACT 668
Qy 532 ACCACCATGGCTGGCACCAAGCCTTACATGTCACCTGAGATGTTTCAGCTCCAGAAAAAGGA 591
Db 669 TGGACCTTGTGCGGACACCTCTGAGTACCTGGCCCTGAGATATCTGAGCAA----- 721
Qy 592 GCAGGCTATTCCTTTGCTGTGACTGGTGGTTCCTCGGAGTGAAGCGGATATGAAGCTG 648
Db 722 --AGGCTCAACAAGAGCGGTGACTGTGTGGCCCTCGGGGTTCTTATCTATGAAGT 776

RESULT 15

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US-09-394-455-5
; Sequence 5, Application US/09394455
; Patent No. 6531305
; GENERAL INFORMATION:
; APPLICANT: Witman, George F.
; APPLICANT: San Agustin, Jovenal
; APPLICANT: Leszyk, John D.
; TITLE OF INVENTION: SPERM ASSOCIATED PROTEIN KINASE POLYPEPTIDES, CORRESPONDING
; TITLE OF INVENTION: NUCLEIC ACIDS, AND METHODS OF USE
; FILE REFERENCE: 07917/078001
; CURRENT APPLICATION NUMBER: US/09/394,455
; CURRENT FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 60/099, 771
; PRIOR FILING DATE: 1998-09-10
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 2549
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (81)...(1133)
; NAME/KEY: misc_feature
; LOCATION: (1)...(2549)
; OTHER INFORMATION: n = A,T,C or G
US-09-394-455-5

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Query Match 11.0%; Score 134.2; DB 4; Length 2549;
Best Local Similarity 54.3%; Pred. No. 5.3e-33;
Matches 324; Conservative 0; Mismatches 258; Indels 15; Gaps 2;
Qy 52 GTCAACTTTTCACACACTTTTGAAATTTTCGGAGCCATTCCGAAAGCGAGTCTTTTGGGAAGTTC 111
Db 195 GCCCAGCTTGATTCAGTTTGTGAACGAATCAAGACCTCTCGGCACGGAGTCTCTTTCCGGCGGGTG 254

112	TGCATTGTACAGAAGATGATACCAAGAGATGTACGCAATGAAGTACATGATATAAACNA	171
Qy		
255	ATGCTGTTGAACAACAAGGAGACCGGGAACCACTATGCCATGAAGATCCTGCACAAACAG	314
Db		
172	AAGTGCCTGGAGCGCAATGAAGTGAAGAAATGCTTTCAAGGAACTCCAGATCATGCAGGGT	231
Qy		
315	AAGTGTGTGAACCTGAACAACAGATCGAACACACACCCCTGAATGAAGCGCATCCTGCAAGCT	374
Db		
232	CTGAGACACCCCTTTCTGTGTTAAATTTGTGGTATTCTTTCCAAGATGAGAGAGACATGTTT	291
Qy		
375	GTCAACTTTTCGGTTCTTCGTCAAACTCGAGTTCTCTTTCAAGGACAACTCAAACTTATAC	434
Db		
292	ATGTTGTTGGACCTCTCTGCTGGGTGGAGACCTCGGTTATCACTTCAACAGAACCTCCAC	351
Qy		
435	ATGTCATGAGTAGCTGCTCCCGCGGGAGATGTTCTCACACCTACGGCGGATCGGAAGG	494
Db		
352	TTCAAGGAAGAAACAGTGAAGCTCTTCAATCTGTGAGCTGGTCAATGGCCCTGAGACTACCTG	411
Qy		
495	TTCACTGAGGCCCATGCCCCGTTTCTACGCGGCCAGATCGCTGACCTTTTGAGTATCTG	554
Db		
412	CAGAAACAGCGCATCATTTCAAGGGATATGAAGCTGACAATATTTTACTTGACGAACAT	471
Qy		
555	CATCTCGCTGGATCTCATCTACAGGACCTGAAGCGGAGATCTGCTCATTTGACCAGAG	614
Db		
472	GGGCACTGTCACATCAAGATTTTCAAATGTCTGGATGTGTCGCCAGGAGACACAGATT	531
Qy		
615	GGCTACATTCAGGTGACAGACTTCGGTTTTCGCCAA-----GCGCGTGAAGGGCGGCAC	668
Db		
532	ACCAACCATGCTGSCACCAAGCCCTTACATGSCACCTGAGATGTTTCAGCTCCAGAAAAAG	591
Qy		
669	TGGACCTTGTGGCGCACCCCTGAGTACTGTGCCCTGAGATTATCCTGAGCNA-----	721
Db		
592	GCAGGCTATTCTTTGCTGTTGACTGTGTGTCCTCGGAGTGAACGGCATATGAAC	648
Qy		
722	--AGGCTACAAAGGCGGTGAACTGTGTGGCCCTGGGGGTTCTTATCTATGAATG	776
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Job time : 94 secs

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OM nucleic - nucleic search, using sw model

Run on: December 20, 2004, 02:02:51 ; Search time 468 Seconds

(without alignments)
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Title: US-10-620-845-8

Perfect score: 1224

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Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: Geneseqn2001s:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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8	1163.8	95.1	1281	12	ADL27076
9	1160.6	94.8	1485	9	ACA62840
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18	660	53.9	678	6	AAD23676
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20	542.4	44.3	3224	4	RAF44625
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22	542.4	44.3	3224	10	ADA19317	Ada19317 Human ins
23	542.4	44.3	3224	10	ACC72764	Acc72764 Human can
24	542.4	44.3	3224	12	ADI29323	Adi29323 Human MAR
25	542.4	44.3	3224	12	ADP07325	Adp07325 Human HSA
26	542.4	44.3	3224	12	ADQ17597	Adq17597 Human sof
27	519.6	42.5	3244	4	AAS46210	Aas46210 Human DNA
28	519.6	42.5	3244	8	ACA89660	Aca89660 cDNA enco
29	519.6	42.5	3244	8	ACA73670	Aca73670 Human sec
30	519.6	42.5	3244	8	ACA05985	Aca05985 Human sec
31	519.6	42.5	3244	8	ACA66819	Aca66819 cDNA enco
32	519.6	42.5	3244	8	ACF20394	Acf20394 Human sec
33	519.6	42.5	3244	8	ACF19780	Acf19780 Human sec
34	519.6	42.5	3244	8	ACD22068	Acd22068 Human sec
35	519.6	42.5	3244	8	ACF11233	Acf11233 Human sec
36	519.6	42.5	3244	8	ACD25336	Acd25336 Human sec
37	519.6	42.5	3244	8	ACF00385	Acf00385 Human sec
38	519.6	42.5	3244	8	ACA72442	ACA72442 Novel hum
39	519.6	42.5	3244	8	ACD04966	Acd04966 Novel hum
40	519.6	42.5	3244	8	ACD18427	Acd18427 Human sec
41	519.6	42.5	3244	8	ACD08434	Acd08434 Human sec
42	519.6	42.5	3244	8	ACA88868	ACA88868 Novel hum
43	519.6	42.5	3244	8	ACA70310	ACA70310 Human sec
44	519.6	42.5	3244	8	ACD12532	Acd12532 Novel hum
45	519.6	42.5	3244	8	ACC74447	Acc74447 Human sec

ALIGNMENTS

RESULT 1						
AAD23678						
ID	AAD23678 standard; cDNA; 1224 BP.					
XX						
AC	AAD23678;					
XX						
DT	07-MAR-2002 (first entry)					
XX						
DE	Novel human protein (NHP) kinase cDNA #3.					
XX						
KW	Novel human protein; NHP; gene therapy; diagnosis; drug screening;					
KW	gene expression; breast cancer; prostate cancer; nutraceutical; cosmetic;					
KW	medical disorder; mental; biological; physiological; chemotherapeutic;					
KW	ss.					
XX						
OS	Homo sapiens.					
XX						
FT	Key					
FT	CDS					
FT	Location/Qualifiers					
FT	1..1224					
FT	/*tag= a					
FT	/product= "Novel human protein (NHP) kinase"					
XX						
PN	WO200181557-A2.					
XX						
PD	01-NOV-2001.					
XX						
PF	24-APR-2001; 2001WO-US013149.					
XX						
PR	25-APR-2000; 2000US-0199499P.					
PR	01-MAY-2000; 2000US-0201227P.					
XX						
PA	(LEXI-) LEXICON GENETICS INC.					
XX						
PI	Hu Y, Nepomnichy B, Wang X, Donoho G, Scoville J, Walke DW;					
XX						
DR	WPI; 2002-034442/04.					
XX						
DR	P-PSDB; AAE14260.					
XX						
PT	New nucleic acid molecules encoding new human proteins, useful in					
PT	diagnosis, drug screening, clinical trial monitoring, treatment of					
XX	physiological disorders, and cosmetic or nutraceutical applications.					
PS	Claim 4; Page 41; 44pp; English.					
XX						

The invention relates to novel human protein (NHP) kinases and their corresponding cDNA molecules. NHP kinase and its DNA are useful as reagents in assays for screening compounds that can be used as pharmaceutical reagents useful in the therapeutic treatment of mental, biological and medical disorders, and also as chemotherapeutic agents useful in the treatment of breast cancer and prostate cancer. NHP DNA is useful for diagnosis, drug screening, clinical trial monitoring, the treatment of physiologic disorders or diseases, and cosmetic and nutraceutical applications. NHP DNA is also useful for the identification of coding sequence and the mapping of a unique gene to a particular chromosome. NHP DNA is further useful as hybridisation probes for screening libraries and assessing gene expression patterns, and also for the detection of mutant NHPs or inappropriately expressed NHPs for disease diagnosis. NHP DNA is also useful in gene therapy. The present sequence is novel human protein (NHP) kinase cDNA which is similar to serine/threonine protein kinases, ribosomal protein kinases and cAMP-dependent kinases cDNA related to the invention

Sequence 1224 BP; 381 A; 263 C; 283 G; 297 T; 0 U; 0 Other;

Query Match	100.0%;	Score 1224;	DE 0;
Best Local Similarity	100.0%;	Pred. No. 0;	Indels
Matches 1224;	Conservative	0;	Mismatches
QY	1	ATGGAGGCAACACACTTCACAGAAAACACACAGTGTTCATGAAATGAAGATGCAACTTT	60
Db	1	ATGGAGGCAACACTTCACAGAAAACACACAGTGTTCATGAAATGAAGATGCAACTTT	60
QY	61	GACCACTTTGAAATTTTTGCGAGCATTTGGGAAGGACGTTTGGGAAGGTCTCCATGTA	120
Db	61	GACCACTTTGAAATTTTTGCGAGCATTTGGGAAGGACGTTTGGGAAGGTCTCCATGTA	120
QY	121	CAGAGAATGATACCAAGAGATGTACGCAATGAAGTACATGAATACAAAGATGCGTG	180
Db	121	CAGAGAATGATACCAAGAGATGTACGCAATGAAGTACATGAATACAAAGATGCGTG	180
QY	181	GAGCGCAATGAAGTCAGAAAATGTTTCAAGAACTCCAGATCATCGAGGCTCTCGAGCAC	240
Db	181	GAGCGCAATGAAGTCAGAAAATGTTTCAAGAACTCCAGAGACTCCAGATCATCGAGGCTCTCGAGCAC	240
QY	241	CTTTTCCTGGTTAATTTGTGTGTTTCCTTCCAAGATGAGGAACATGTTTCATGTGGTG	300
Db	241	CTTTTCCTGGTTAATTTGTGTGTTTCCTTCCAAGATGAGGAACATGTTTCATGTGGTG	300
QY	301	GACCTCTGCTGGGTGGAGACCTGGGTTATCACTCTGCAACAGAACTGCCACTTCAAGAA	360
Db	301	GACCTCTGCTGGGTGGAGACCTGGGTTATCACTCTGCAACAGAACTGCCACTTCAAGAA	360
QY	361	GAACACAGTGAAGCTTTTCATCTGTGAGCTGGTCATGGCCCTGGACCTACCTGCAGAACAC	420
Db	361	GAACACAGTGAAGCTTTTCATCTGTGAGCTGGTCATGGCCCTGGACCTACCTGCAGAACAC	420
QY	421	CGCATCTTACACAGGATATGAAGCCTGACATATTTTACTTTGACACACATGGGCACGTG	480
Db	421	CGCATCTTACACAGGATATGAAGCCTGACATATTTTACTTTGACACACATGGGCACGTG	480
QY	481	CACATCACAGATTTCAACATTTGCTGCGATGCTGCCAGGAGACACAGATTCACCACTG	540
Db	481	CACATCACAGATTTCAACATTTGCTGCGATGCTGCCAGGAGACACAGATTCACCACTG	540
QY	541	GCTGGCACCAAGCCTTACATGCGACCTGAGATGTTCAAGTCCAGAAAAGGACGCGCTAT	600
Db	541	GCTGGCACCAAGCCTTACATGCGACCTGAGATGTTCAAGTCCAGAAAAGGACGCGCGG	660
QY	601	TCCCTTTCCTGTTTCACCTGCTGGTCCCTGGGAGTGAAGGCATATGAACTGTCGAGCGCGG	660
Db	601	TCCCTTTCCTGTTTCACCTGCTGGTCCCTGGGAGTGAAGGCATATGAACTGTCGAGCGCGG	720
QY	661	AGACCGTATCATATTTGCTCCAGTACTTCCAGCAAGGAAATTTGACACAGCTTTGAGACG	720
Db	661	AGACCGTATCATATTTGCTCCAGTACTTCCAGCAAGGAAATTTGACACAGCTTTGAGACG	720
QY	721	ACTGTTGTTAACTTACCTTCTGCTGGTCCAGGAAATTTGGTGTCACTTCTTAAAGACCTA	780

Db	721	ACTGTTGAACCTTACCCCTTCTGCTGGTCCAGGAATGCTGCTTCTTAAAAAGCTA	780
Qy	781	CTCGAACCTTAATCCAGACAACGATTTTCTCAGTTATCTGATGTCAGAACTTCCCGTAT	840
Db	781	CTCGAACCTTAATCCAGACAACGATTTTCTCAGTTATCTGATGTCAGAACTTCCCGTAT	840
Qy	841	ATGAATGATATAAACTGGGATCGAGTTTTTCAGAAGAGGCTCATTCAGGTTTCATTCCT	900
Db	841	ATGAATGATATAAACTGGGATCGAGTTTTTCAGAAGAGGCTCATTCAGGTTTCATTCCT	900
Qy	901	AATAAAGCGCAGGCTGAATGTGATCTCTACTCTTGAACCTTGAGAAATGATTTTGGAGTCC	960
Db	901	AATAAAGCGCAGGCTGAATGTGATCTCTACTCTTGAACCTTGAGAAATGATTTTGGAGTCC	960
Qy	961	AAACCTCTACATAAGAAAAAGAAAAAGCGCTGGCAAGAGGAGGATATGAGGAAATGC	1020
Db	961	AAACCTCTACATAAGAAAAAGAAAAAGCGCTGGCAAGAGGAGGATATGAGGAAATGC	1020
Qy	1021	GAATCTTCTCAGACATGCTCTTTCAAGAGCAGCTTGAATCTGTCTCAGAGGAGTTTCATA	1080
Db	1021	GAATCTTCTCAGACATGCTCTTTCAAGAGCAGCTTGAATCTGTCTCAGAGGAGTTTCATA	1080
Qy	1081	ATTTTCAACAGAGAAAAAGTAAACAGGGACTTTAAACAAAAGACAACAAATCTAGCCTTG	1140
Db	1081	ATTTTCAACAGAGAAAAAGTAAACAGGGACTTTAAACAAAAGACAACAAATCTAGCCTTG	1140
Qy	1141	GAACAAACCAAAGACCCACAAGTGAACAAATGGACACAGGACCTCAGTGAGACT	1200
Db	1141	GAACAAACCAAAGACCCACAAGTGAACAAATGGACACAGGACCTCAGTGAGACT	1200
Qy	1201	TTTTCAGACCTCGAAAGTTTCATAA	1224
Db	1201	TTTTCAGACCTCGAAAGTTTCATAA	1224

RESULT 2

AAD23680	
ID	AAD23680 standard; DNA; 1675 BP.
XX	
AC	AAD23680;
XX	
DT	07-MAR-2002 (first entry)
XX	
XX	Novel human protein (NHP) kinase full-length ORF and flanking region DNA.
DE	
XX	Novel human protein; NHP; gene therapy; diagnosis; drug screening;
KW	gene expression; breast cancer; prostate cancer; nutraceutical; cosmetic;
KW	medical disorder; mental; biological; physiological; chemotherapeutic;
KW	ds.
XX	
OS	Homo sapiens.
XX	
PN	WO200181557-A2.
XX	
PD	01-NOV-2001.
XX	
EF	24-APR-2001; 2001WO-US013149.
XX	
PR	25-APR-2000; 2000US-0199499P.
PR	01-MAY-2000; 2000US-0201227P.
XX	
PA	(LEXI-) LEXICON GENETICS INC.
XX	
XX	Hu Y, Nepomnichy B, Wang X, Donoho G, Scoville J, Walke DW;
PI	
XX	WPI; 2002-034442/04.
DR	
XX	New nucleic acid molecules encoding new human proteins, useful in
PT	diagnosis, drug screening, clinical trial monitoring, treatment of
PT	physiological disorders, and cosmetic or nutraceutical applications.
PS	Disclosure; Page 44; 44pp; English.

disclosure: page 44; 44pp; English.

XX SD

XX The invention relates to novel human protein (NHP) kinases and their
 CC corresponding cDNA molecules. NHP kinase and its DNA are useful as
 CC reagents in assays for screening compounds that can be used as
 CC pharmaceutical reagents useful in the therapeutic treatment of mental,
 CC biological and medical disorders, and also as chemotherapeutic agents
 CC useful in the treatment of breast cancer and prostate cancer. NHP DNA is
 CC useful for diagnosis, drug screening, clinical trial monitoring, the
 CC treatment of physiological disorders or diseases, and cosmetic and
 CC nutraceutical applications. NHP DNA is also useful for the identification
 CC of coding sequence and the mapping of a unique gene to a particular
 CC chromosome. NHP DNA is further useful as hybridisation probes for
 CC screening libraries and assessing gene expression patterns, and also for
 CC the detection of mutant NHPs or inappropriately expressed NHPs for
 CC disease diagnosis. NHP DNA is also useful in gene therapy. The present
 CC sequence is novel human protein (NHP) kinase full-length ORF (open
 CC reading frame) and flanking region DNA related to the invention
 XX
 SQ Sequence 1675 BP; 469 A; 404 C; 414 G; 388 T; 0 U; 0 Other;

Query Match 100.0%; Score 1224; DB 6; Length 1675;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGGAGCCAACTTCAAGAAACCCACCTGTTTGTATGAATAATGAAGATGTCAACTTT 60
 Db |||||
 QY 413 ATGGGAGCCAACTTCAAGAAACCCACCTGTTTGTATGAATAATGAAGATGTCAACTTT 472
 Db |||||
 QY 61 GACCACCTTTGAAATTTTCGAGCCATTGGGAAAGCGAGTTTGGGAAAGTCTGCAATTGTA 120
 Db |||||
 QY 473 GACCACCTTTGAAATTTTCGAGCCATTGGGAAAGCGAGTTTGGGAAAGTCTGCAATTGTA 532
 Db |||||
 QY 121 CAGAAGATGATACCAAGAAGATGACCAATGAAGTACATGAATAACAAGAGTGGGTG 180
 Db |||||
 QY 533 CAGAAGATGATACCAAGAAGATGACCAATGAAGTACATGAATAACAAGAGTGGGTG 592
 Db |||||
 QY 181 GAGCGCAATGAAGTGAGAAATGCTTCAAGAACTCCAGATCATGCGGGTCTCGAGCAC 240
 Db |||||
 QY 593 GAGCGCAATGAAGTGAGAAATGCTTCAAGAACTCCAGATCATGCGGGTCTCGAGCAC 652
 Db |||||
 QY 241 CCTTTCCTGGTTAATTTTGGTGTATTCCTTCAAGATGAGGAAGACATGTTTCATGGTGTG 300
 Db |||||
 QY 653 CCTTTCCTGGTTAATTTTGGTGTATTCCTTCAAGATGAGGAAGACATGTTTCATGGTGTG 712
 Db |||||
 QY 301 GACCTCTCTGGTGGAGACCTGGTTATCACTGCAACAGACCTTCACTTCAAGGAA 360
 Db |||||
 QY 713 GACCTCTCTGGTGGAGACCTGGTTATCACTGCAACAGACCTTCACTTCAAGGAA 772
 Db |||||
 QY 361 GAAACAGTGAAGCTTTCATCTGTGAGCTGTGATGCGCCCTGGACTACCTGCAGAACCG 420
 Db |||||
 QY 773 GAAACAGTGAAGCTTTCATCTGTGAGCTGTGATGCGCCCTGGACTACCTGCAGAACCG 832
 Db |||||
 QY 421 CGCATCTTCAAGGATATGAAGCTTCAATATTTTACTTTGAGCAATCGGCAGCTG 480
 Db |||||
 QY 833 CGCATCTTCAAGGATATGAAGCTTCAATATTTTACTTTGAGCAATCGGCAGCTG 892
 Db |||||
 QY 481 CACATCAGATTTCAACATTTCTGCGATGCTGCCAGGGAGACACAGATTACCAACATG 540
 Db |||||
 QY 893 CACATCAGATTTCAACATTTCTGCGATGCTGCCAGGGAGACACAGATTACCAACATG 952
 Db |||||
 QY 541 CTTGGCACCAGCCTTACATGCGCCTCAGATGTTTCAGCTCCAGAAAGGAGCGGCTAT 600
 Db |||||
 QY 953 CTTGGCACCAGCCTTACATGCGCCTCAGATGTTTCAGCTCCAGAAAGGAGCGGCTAT 1012
 Db |||||
 QY 601 TCTTTTGTGTTGACTGTGGTTCCTCTGGAGTGACGGCATATGAATCTGCTGAGAGCCGG 660
 Db |||||
 QY 1013 TCTTTTGTGTTGACTGTGGTTCCTCTGGAGTGACGGCATATGAATCTGCTGAGAGCCGG 1072
 Db |||||
 QY 661 AGACCGTATCATATTCGCTCCAGTACTTCCAGCAGAGGAAATTTGTACACAGTTTGAGACG 720
 Db |||||
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 Db |||||
 QY 721 ACTGTTGTAACCTTACCCCTTCTGCGCTGGTGCACAGGAAATGGTGTCACTTCTTAAAGGCTA 780
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 QY 1133 ACTGTTGTAACCTTACCCCTTCTGCTGCTGCACAGGAAATGGTGTCACTTCTTAAAGGCTA 1192
 QY 781 CTGGAACCTTAATCAGACCAACGATTTTCTCAGTTATCTGATGTCCAGAACTTCCCGTAT 840
 Db |||||
 QY 1193 CTGGAACCTTAATCAGACCAACGATTTTCTCAGTTATCTGATGTCCAGAACTTCCCGTAT 1252
 QY 841 ATGAATCATATAAAGCTGGGATGCAATTTTTCAGAAAGGCTCATTTCCAGGTTTTCATTCCT 900
 Db |||||
 QY 1253 ATGAATCATATAAAGCTGGGATGCAATTTTTCAGAAAGGCTCATTTCCAGGTTTTCATTCCT 1312
 QY 901 AATAAAGCGAGGCTGAATTTGTGATCTCTTCAAGAGCCTTTCAGGAAATGATTTTGGAGTCC 960
 Db |||||
 QY 1313 AATAAAGCGAGGCTGAATTTGTGATCTCTTCAAGAGCCTTTCAGGAAATGATTTTGGAGTCC 1372
 QY 961 AAACCTCTACATAAGAAAAAGCGCTCTGCAAGAGGAGGAGATATGAGGAAATGC 1020
 Db |||||
 QY 1373 AAACCTCTACATAAGAAAAAGCGCTCTGCAAGAGGAGGAGATATGAGGAAATGC 1432
 QY 1021 GATTTCTTCTCAGACATGCTTCTTCAAGAGCCTTTCAGTCTGCTCCAGAGGAGTTCATA 1080
 Db |||||
 QY 1433 GATTTCTTCTCAGACATGCTTCTTCAAGAGCCTTTCAGTCTGCTCCAGAGGAGTTCATA 1492
 QY 1081 ATTTTCAACAGAGAAAAAGTAAACAGGGACCTTTTAAACAAAAGACAAACCAATCTAGCCTTG 1140
 Db |||||
 QY 1493 ATTTTCAACAGAGAAAAAGTAAACAGGGACCTTTTAAACAAAAGACAAACCAATCTAGCCTTG 1552
 QY 1141 GAACAAACCAAGACCCACAAAGTGACAAATGGACAAATGGACACAGGACTCAGTGAGACT 1200
 Db |||||
 QY 1553 GAACAAACCAAGACCCACAAAGTGACAAATGGACAAATGGACACAGGACTCAGTGAGACT 1612
 QY 1201 TTTTCAGACCTCGAAGTTTCATA 1224
 Db |||||
 QY 1613 TTTTCAGACCTCGAAGTTTCATA 1636
 Db |||||

RESULT 3
 AAD23679
 ID AAD23679 standard; cDNA; 1191 BP.
 XX
 AC AAD23679;
 XX
 DT 07-MAR-2002 (first entry)
 XX
 DE Novel human protein (NHP) kinase cDNA #4.
 DE Novel human protein; NHP; gene therapy; diagnosis; drug screening;
 KW gene expression; breast cancer; prostate cancer; nutraceutical; cosmetic;
 KW medical disorder; mental; biological; physiological; chemotherapeutic;
 KW ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..1191
 FT /*tag= a
 FT /product= "Novel human protein (NHP) kinase"
 XX
 FN WO200181557-A2.
 XX
 PD 01-NOV-2001.
 XX
 PF 24-APR-2001; 2001WO-US013149.
 XX
 PR 25-APR-2000; 2000US-0199499P.
 XX
 PR 01-MAY-2000; 2000US-0201227P.
 XX
 XX (LEXI-) LEXICON GENETICS INC.
 PA
 XX Hu Y, Nepomnichy B, Wang X, Donoho G, Scoville J, Walke DW;
 PI WPI; 2002-034442/04.
 DR P-FSDB; AAE14261.

XX New nucleic acid molecules encoding new human proteins, treatment in
PT diagnosis, drug screening, clinical trial monitoring, treatment of
PT physiological disorders, and cosmetic or nutraceutical applications.
XX Claim 7; Page 42; 44pp; English.

XX The invention relates to novel human protein (NHP) kinases and their
CC corresponding cDNA molecules. NHP kinase and its DNA are useful as
CC reagents in assays for screening compounds that can be used as
CC pharmaceutical reagents useful in the therapeutic treatment of mental,
CC biological and medical disorders, and also as chemotherapeutic agents
CC useful in the treatment of breast cancer and prostate cancer. NHP DNA is
CC useful for diagnosis, drug screening, clinical trial monitoring, the
CC treatment of physiological disorders or diseases, and cosmetic and
CC nutraceutical applications. NHP DNA is also useful for the identification
CC of coding sequence and the mapping of a unique gene to a particular
CC chromosome. NHP DNA is further useful as hybridisation probes for
CC screening libraries and assessing gene expression patterns, and also for
CC the detection of mutant NHPs or inappropriately expressed NHPs for
CC disease diagnosis. NHP DNA is also useful in gene therapy. The present
CC sequence is novel human protein (NHP) kinase cDNA which is similar to
CC serine/threonine protein kinases, ribosomal protein kinases and CAMP-
CC dependent kinases cDNA related to the invention

XX Sequence 1191 BP; 369 A; 254 C; 278 G; 290 T; 0 U; 0 Other;

Query Match 95.2%; Score 1165.4; DB 6; Length 1191;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 1172; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 ATGGAGGCCAACACTTCAAGAAACACCACGAGTGTGATGAATGAAGATGTCAACTTT 60
DB 1 ATGGAGGCCAACACTTCAAGAAACACCACGAGTGTGATGAATGAAGATGTCAACTTT 60

QY 61 GACCACTTTGAATTTGGAGCCATTTGGAAAGGCGATTTTGGAAAGGCTGCAATGTA 120
DB 61 GACCACTTTGAATTTGGAGCCATTTGGAAAGGCGATTTTGGAAAGGCTGCAATGTA 120

QY 121 CAGAAGATGATACCAAGAGATGATGACCAATGAATGATGATGATGATGATGATGATG 180
DB 121 CAGAAGATGATACCAAGAGATGATGACCAATGAATGATGATGATGATGATGATGATG 180

QY 181 GAGCGCAATGAAGTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 240
DB 181 GAGCGCAATGAAGTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 240

QY 241 CTTTCTCTGTTAATTTGTTGTTATTTCTTCAAGATGATGATGATGATGATGATGATG 300
DB 241 CTTTCTCTGTTAATTTGTTGTTATTTCTTCAAGATGATGATGATGATGATGATGATG 300

QY 301 GACCTCTCTGTTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 360
DB 301 GACCTCTCTGTTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 360

QY 361 GAAACAGTGAAGCTCTTCACTGTGAGCTGTTGATGATGATGATGATGATGATGATG 420
DB 361 GAAACAGTGAAGCTCTTCACTGTGAGCTGTTGATGATGATGATGATGATGATGATG 420

QY 421 CGCATCTTACAGGGATGATGAGCTGATGATGATGATGATGATGATGATGATGATG 480
DB 421 CGCATCTTACAGGGATGATGAGCTGATGATGATGATGATGATGATGATGATGATG 480

QY 481 CACATCAGAGATTTCAATGTTGCTGCTGATGCTGCCAGGAGACACAGATTACCCCATG 540
DB 481 CACATCAGAGATTTCAATGTTGCTGCTGATGCTGCCAGGAGACACAGATTACCCCATG 540

QY 541 GCTGSCACCAAGCCCTTACATGCGACCTGAGATGTTTCACTCCAGAAAGGAGGAGGCTAT 600
DB 541 GCTGSCACCAAGCCCTTACATGCGACCTGAGATGTTTCACTCCAGAAAGGAGGAGGCTAT 600

QY 601 TCCCTTGTCTGTTGATGTTGCTGCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 660
DB 601 TCCCTTGTCTGTTGATGTTGCTGCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 660

Db 601 TCCCTTGTCTGTTGATGTTGCTGCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 660
QY 661 AGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGCAAAATGTACACACGTTTGAGACG 720
Db 661 AGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGCAAAATGTACACACGTTTGAGACG 720
QY 721 ACTGTTGTAATTAACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
Db 721 ACTGTTGTAATTAACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
QY 781 CTCGAACCTAATCCAGACCAACGATTTTCTCAGTATCTGATGTCAGAACTTCCCGTAT 840
Db 781 CTCGAACCTAATCCAGACCAACGATTTTCTCAGTATCTGATGTCAGAACTTCCCGTAT 840
QY 841 ATGAATGATATAAACTGGGATGCAATTTTTCAGAAAGGCTCATTTCCAGGTTTCATTCCT 900
Db 841 ATGAATGATATAAACTGGGATGCAATTTTTCAGAAAGGCTCATTTCCAGGTTTCATTCCT 900
QY 901 AATAAAGCGCAGGCTGAATTTGTGATCTTCACTTTTGAACCTTGAGGAAATGATTTTGGAGTCC 960
Db 901 AATAAAGCGCAGGCTGAATTTGTGATCTTCACTTTTGAACCTTGAGGAAATGATTTTGGAGTCC 960
QY 961 AAACCTCTACATAAGAAAAAAGCGCTGCGCAAGAGGAGGAGGATATGAGAAATGC 1020
Db 961 AAACCTCTACATAAGAAAAAAGCGCTGCGCAAGAGGAGGAGGATATGAGAAATGC 1020
QY 1021 GATTTCTTCTCAGACATGCTTCTTCAAGAGCAGCTTCACTCTGTCAGAGAGGAGTTCATA 1080
Db 1021 GATTTCTTCTCAGACATGCTTCTTCAAGAGCAGCTTCACTCTGTCAGAGAGGAGTTCATA 1080
QY 1081 ATTTTCAACGAGAAAAAAGTAAACAGGAGCTTTTAAACAAAAAGACAAACCAATCTAGCCTTG 1140
Db 1081 ATTTTCAACGAGAAAAAAGTAAACAGGAGCTTTTAAACAAAAAGACAAACCAATCTAGCCTTG 1140
QY 1141 GAACAAACCAAGACCCCAAGTGACAAATGGACAAATGGACA 1183
Db 1141 GAACAAACCAAGACCCCAAGTGAGGATGGTGCAGAAATAACA 1183

RESULT 4
AAH46891 ID AAH46891 standard; cDNA; 1594 BP.
XX AC AAH46891;
DT 25-SEP-2001 (first entry)
XX cDNA encoding human protein kinase SGK177.
DE Protein kinase; enzyme; cytostatic; nootropic; neuroprotective; human;
KW antiparkinsonian; viricide; antibacterial; antifungal; antimigraine;
KW analgesic; hypotensive; viricide; hypertensive; immunosuppressive; antiallergic;
KW antiparkinsonian; antirheumatic; antidiabetic; antihypertensive; anorectic;
KW osteopathic; thrombolytic; antidiabetic; antihypertensive; antidiabetic;
KW vasotrophic; antidiabetic; gene therapy; ss.
XX Homo sapiens.
XX Key Location/Qualifiers
CDS 404..1594
FT /*tag= a
FT WO200155356-A2.
XX PD 02-AUG-2001.
XX PF 25-JAN-2001; 2001WO-US002337.
XX PR 25-JAN-2000; 2000US-0178078P.
XX PR 31-JAN-2000; 2000US-0179364P.
XX PR 17-FEB-2000; 2000US-0183173P.
XX PR 17-MAR-2000; 2000US-0190162P.
XX PR 29-MAR-2000; 2000US-0193404P.


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FT CDS 404..1594
FT /*tag= a
FT /product= "Human PKIN-20 protein"
XX
XX WO200218557-A2.
XX
XX PD
XX PF
XX PF 31-AUG-2001; 2001WO-US027219.
XX
XX PR 31-AUG-2000; 2000US-0229873P.
XX PR 08-SEP-2000; 2000US-0231357P.
XX PR 14-SEP-2000; 2000US-0232654P.
XX PR 22-SEP-2000; 2000US-0234902P.
XX PR 29-SEP-2000; 2000US-0236499P.
XX PR 06-OCT-2000; 2000US-0238389P.
XX PR 13-OCT-2000; 2000US-0240542P.
XX
XX (INCY-) INCYTE GENOMICS INC.
XX
XX PI Bandman O, Nguyen DB, Walia NK, Hafalia AJA, Yao MG, Gandhi AR,
PI Gururajan R, Ding L, Patterson C, Yue H, Baughn MR, Tribouley CM,
PI Thornton M, Elliott VS, Lu Y, Ison CH, Au-Young J, Tang YT,
PI Azimzai Y, Burrill JD, Marcus GA, Zingler KA, Lu DAM, Lal PG,
PI Ramkumar J, Warren BA, Kearney L, Policky JL, Thangavelu K,
PI Burford N;
XX
XX WPI; 2002-329769/36.
XX P-PSDB; ABE21725.
XX
XX New human kinases, useful for diagnosing, treating or preventing immune
XX system disorders (e.g. Crohn's disease), neurological disorders (e.g.
XX epilepsy), or cell proliferative disorders (e.g. cancers such as leukemia
XX or lymphoma).
XX
XX Claim 99; Page 214; 218pp; English.
XX
XX The present invention relates to human kinases (PKIN) and polynucleotides
XX encoding such proteins. PKIN sequences of the invention are useful for
XX diagnosing, treating or preventing disorders associated with aberrant
XX expression of PKIN, particularly immune system disorders (e.g. acquired
XX immune deficiency syndrome (AIDS), thymic hypoplasia, Crohn's disease,
XX anaemia, asthma), neurological disorders (e.g. epilepsy, Charcot-Marie-
XX Tooth disease or seizures), cell proliferative disorders (e.g. cancers
XX such as adenocarcinoma, leukaemia, lymphoma, melanoma, myeloma, sarcoma),
XX and developmental disorders (e.g. Down's syndrome). They are also used in
XX gene therapy and protein therapy. The present sequence is a cDNA encoding
XX human PKIN-20 protein
XX
XX Sequence 1594 BP; 441 A; 386 C; 395 G; 372 T; 0 U; 0 Other;
XX
XX Query Match 95.2%; Score 1165.4; DB 6; Length 1594;
XX Best Local Similarity 99.1%; Pred. No. 0;
XX Matches 1172; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
XX
XX QY 1 ATGGAGGCAACACATTCGAAGAAACCCACGAGTGTGTGATGAATAATGAAGATGTCAACTTT 60
XX DB 404 ATGGAGGCAACACATTCGAAGAAACCCACGAGTGTGTGATGAATAATGAAGATGTCAACTTT 463
XX
XX QY 61 GACCACTTTGAAATTTGGAGGCCATTGGGAAAGCCAGTTTGGGAAAGGCTCGCATTTGTA 120
XX DB 464 GACCACTTTGAAATTTGGAGGCCATTGGGAAAGCCAGTTTGGGAAAGGCTCGCATTTGTA 523
XX
XX QY 121 CAGAAGAATGATACCAAGAAGATGTACCAATGAAGTACATGAATAAACAAGTGCGTG 180
XX DB 524 CAGAAGAATGATACCAAGAAGATGTACCAATGAAGTACATGAATAAACAAGTGCGTG 583
XX
XX QY 181 GAGCGCAATGAAGTGAAGAAATGTCTTCAAGGAACCTCCAGATCATGCAGGGTCTGGAGCAC 240
XX DB 584 GAGCGCAATGAAGTGAAGAAATGTCTTCAAGGAACCTCCAGATCATGCAGGGTCTGGAGCAC 643
XX
XX QY 241 CCTTTCCTGGTTAATTTGGTGTATTCCTTCCAGATGAGGAAGACATGTTTCATGGTGTG 300
XX

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RESULT 6
ADL27078
ID ADL27078 standard; cDNA; 1191 BP.
XX
AC ADL27078;
XX
DT 20-MAY-2004 (first entry)
XX
DE Novel human DNA molecule, 14911.
XX

```

Db 644 CTTTTCCTGGTTAATTTGGTGTATTCCTTCAAGATGAGGAAGACATGTTTCATGGTGTG 703
QY 301 GACCTCTCTGGTGGAGACCTCGTTATCACCTGCAACAGAAACGCTCCACTTCAAGGAA 360
Db 704 GACCTCTCTGGTGGAGACCTCGTTATCACCTGCAACAGAAACGCTCCACTTCAAGGAA 763
QY 361 GAAACAGTGAAGCTCTTTCATCTGTGAGCTGTGTCAATGGCCCTGGACTACCTGCGAAC 420
Db 764 GAAACAGTGAAGCTCTTTCATCTGTGAGCTGTGTCAATGGCCCTGGACTACCTGCGAAC 823
QY 421 GGCATCATTCACAGGGATATGAAGCCTTGACAAATATTTTACCTGACGACATGCGACG 480
Db 824 GGCATCATTCACAGGGATATGAAGCCTTGACAAATATTTTACCTGACGACATGCGACG 883
QY 481 CACATCACAGATTTCAACATTTGCTGCGATGCTGCCAGGGAGACACAGATTTACCA 540
Db 884 CACATCACAGATTTCAACATTTGCTGCGATGCTGCCAGGGAGACACAGATTTACCA 943
QY 541 GCTGGCAACCAAGCCTTACATGGCACCTTGAGATGTTTCAAGTCCAGAAAGGAGCGGTAT 600
Db 944 GCTGGCAACCAAGCCTTACATGGCACCTTGAGATGTTTCAAGTCCAGAAAGGAGCGGTAT 1003
QY 601 TCCTTTGCTGTGACTGGTGTGCTCGGAGTGACGCATATGAACTGCTGAGAGGCGG 660
Db 1004 TCCTTTGCTGTGACTGGTGTGCTCGGAGTGACGCATATGAACTGCTGAGAGGCGG 1063
QY 661 AGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAAATTTGACACACACGTTTGAGACG 720
Db 1064 AGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAAATTTGACACACGTTTGAGACG 1123
QY 721 ACTGTTGTAATTAACCTTCTGCTGTGCTCAGGAAATGTTGTCATCTTTAAAGGCTA 780
Db 1124 ACTGTTGTAATTAACCTTCTGCTGTGCTCAGGAAATGTTGTCATCTTTAAAGGCTA 1183
QY 781 CTCGAACCTTAATCCAGACCAAGGAAATTTCTCAGTATCTGATGTCGAGAACTTCCCGTAT 840
Db 1184 CTCGAACCTTAATCCAGACCAAGGAAATTTCTCAGTATCTGATGTCGAGAACTTCCCGTAT 1243
QY 841 ATGAATGATATAAACTGGGATGCAAGTATTTTTCAGAAAGGCTCATTTCCAGGTTTCAATTCCT 900
Db 1244 ATGAATGATATAAACTGGGATGCAAGTATTTTTCAGAAAGGCTCATTTCCAGGTTTCAATTCCT 1303
QY 901 AATAAAGCAGGCTGAATTTGTGATCTTCACTTGAACCTTGAGGAAATGATTTTGGAGTCC 960
Db 1304 AATAAAGCAGGCTGAATTTGTGATCTTCACTTGAACCTTGAGGAAATGATTTTGGAGTCC 1363
QY 961 AAACCTCTACATAGAATAAAGGCTCTGCAAGGAGGAGGAGGATATGAGGAATGC 1020
Db 1364 AAACCTCTACATAGAATAAAGGCTCTGCAAGGAGGAGGAGGATATGAGGAATGC 1423
QY 1021 GATTTCTTCTCAGACATGTTCTTCTTCAAGAGCACCTTGACTCTGTCAGAGAGGAGTTCATA 1080
Db 1424 GATTTCTTCTCAGACATGTTCTTCTTCAAGAGCACCTTGACTCTGTCAGAGAGGAGTTCATA 1483
QY 1081 ATTTTCAACAGAGAAAAAGTAAACAGGACCTTTTAAACAAAAGACAAACCAAAATCTAGCCTTG 1140
Db 1484 ATTTTCAACAGAGAAAAAGTAAACAGGACCTTTTAAACAAAAGACAAACCAAAATCTAGCCTTG 1543
QY 1141 GAACAAACCAAGAACCCACAGTCAACAATGGACAAATGGACA 1183
Db 1544 GAACAAACCAAGAACCCACAGTGGATGGTTCAGAAATAACA 1586

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Db	889	ATGAATGATATAAACTGGATGCACTTTTTTCAGAAGAGGCTCATCTTCAGGTTTCATTCCT	948
Qy	901	AATAAAGCGCAGGCTGAATTGTGATCTCACTTTGAACTTGAGGAAATGATTTTGGAGTCC	960
Db	949	AATAAAGCGCAGGCTGAATTGTGATCTCACTTTGAACTTGAGGAAATGATTTTGGAGTCC	1008
Qy	961	AAACCTCTACATAGAAAAAAGCGCTCGCAAAGAGGAGGAGGATATGAGGAATGC	1020
Db	1009	AAACCTCTACATAGAAAAAAGCGCTCGCAAAGAGGAGGAGGATATGAGGAATGC	1068
Qy	1021	GATCTCTTCAGACATCTCTTTCAAGAGCACCTTCGCTCTGCCAAGAGGAGTTTCATA	1080
Db	1069	GATCTCTTCAGACATCTCTTTCAAGAGCACCTTCGCTCTGCCAAGAGGAGTTTCATA	1128
Qy	1081	ATTTTCAACAGAGAAAAAGTAAACAGAGCATTTTAAACAAGACACCAAAATCTAGCCTTG	1140
Db	1129	ATTTTCAACAGAGAAAAAGTAAACAGAGCATTTTAAACAAGACACCAAAATCTAGCCTTG	1188
Qy	1141	GAACAAACCAAAGACCCCAAGTGACAAATGGACAAATGGACA	1183
Db	1189	GAACAAACCAAAGACCCCAAGGTGAGCATGGTTCAGAAATACCA	1231

PI Meyers RE, Macbeth KJ, Curtis RAJ, Rudolph-Owen LA, Weich NS;
 PI Olandt PJ, Tsai F, Kapeller-Libermann R, Carroll JW;
 XX WPI: 2004-081724/08.
 DR P-PSDB: ADL27077.
 XX
 XX
 PT New isolated 26199, 33530, 33949, 47148, 50226, 58764, 62113, 32144,
 PT 32235, 23565, 13305, 14911, 86216, 25206 or 8843 polypeptides and nucleic
 PT acids, useful for diagnosing or treating cancer, autoimmune, metabolic
 PT and viral diseases.
 XX
 XX
 PS Claim 2; SEQ ID NO 100; 237pp; English.
 XX
 CC The invention relates to novel nucleic acid molecules designated 26199,
 CC 33530, 33949, 47148, 50226, 58764, 62113, 32144, 32235, 23565, 13305,
 CC 14911, 86216, 25206 or 8843. The novel nucleic acid molecules and their
 CC compositions have the following activities: cytostatic, haemostatic,
 CC gynecological, nephrotropic, dermatological, immunosuppressive,
 CC antiinflammatory, hepatotropic, virucide, analgesic, and vasotropic. The
 CC novel nucleic acid molecules may be used in gene therapy top treat
 CC disorders. The methods and compositions of the present invention are
 CC useful for the diagnosis, prevention and/or treatment of diseases or
 CC conditions associated with aberrant expression or activity of the
 CC polypeptides, such as a cellular proliferative and/or differentiative
 CC disorder, brain disorder, platelet disorder, breast disorder, colon
 CC disorder, kidney (renal) disorder, lung disorder, ovarian disorder,
 CC prostate disorder, haematopoietic disorder, pancreatic disorder, skeletal
 CC muscle disorder, skin (dermal) disorder, disorder associated with bone
 CC metabolism, immune, e.g., inflammatory, disorder, cardiovascular
 CC disorder, endothelial cell disorder, liver disorder, viral diseases, pain
 CC disorder, metabolic disorder, neurological or CNS disorder, erythroid
 CC disorder or anemic disorder. The compositions may also be used in assays
 CC to identify other proteins or molecules involved in binding reaction, to
 CC generate transgenic animals or knockout animals, which in turn are useful
 CC in the development and screening of therapeutically useful reagents, for
 CC chromosome identification, and tissue typing. This polynucleotide
 CC sequence represents one of the novel human nucleic acid molecules of the
 CC invention.
 XX
 SQ Sequence 1281 BP; 392 A; 277 C; 299 G; 313 T; 0 U; 0 Other;

Query Match	95.1%	Score 1163.8;	DB 12;	Length 1281;
Best Local Similarity	99.0%;	Pred. No. 0;		
Matches 1171;	Conservative 0;	Mismatches 12;	Indels 0;	Gaps 0;
Qy	1	ATGGGAGCCAACTTTCAAGAAAAACACCACTGTTTTCATGAAAAATGAAGATGTCAACTTT	60	
Db	49	ATGGGAGCCAACTTTCAAGAAAACCCACCACTGTTTTCATGAAAATGAAGATGTCAACTTT	108	
Qy	61	GACCACTTTGAAATTTTGGAGCCATTTGGAAAAGGCAGTTTGGGAAGGTCTGCATTGTA	120	
Db	109	GACCACTTTGAAATTTTGGAGCCATTTGGAAAAGGCAGTTTGGGAAGGTCTGCATTGTA	168	
Qy	121	CAGAAGAAATGATACCAAGAAGATGTACGCAATGAAAGTACATGAATAAACAAAAGTGCCTG	180	
Db	169	CAGAAGAAATGATACCAAGAAGATGTACGCAATGAAAGTACATGAATAAACAAAAGTGCCTG	228	
Qy	181	GAGCGCAATGAGTGAGAAATGCTTTCAGGAACCTCCAGATCATGCAGGCTCGGAGCAC	240	
Db	229	GAGCGCAATGAGTGAGAAATGCTTTCAGGAACCTCCAGATCATGCAGGCTCGGAGCAC	288	
Qy	241	CTTTTCCTGGTTAAATTTGTGTTATTCCTTCCAAGATGAGGAAGACATGTTTCATGGTGGTG	300	
Db	289	CTTTTCCTGGTTAAATTTGTGTTATTCCTTCCAAGATGAGGAAGACATGTTTCATGGTGGTG	348	
Qy	301	GACCTCCTGCTGGTGGAGACCTGCGTTATCACTGCACAGAAAGTCCACTTCMAGGAA	360	
Db	349	GACCTCCTGCTGGTGGAGACCTGCGTTATCACTGCACAGAAAGTCCACTTCMAGGAA	408	
Qy	361	GAAACAGTGAAGCTTTTCATCTGTGAGCTGGTCATGGCCCTGGACTACCTGCGAGAACCG	420	
Db	409	GAAACAGTGAAGCTTTTCATCTGTGAGCTGGTCATGGCCCTGGACTACCTGCGAGAACCG	468	

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QY 421 CGCATCAITTCACAGGATATGAAGCCTGCAATATTTTACTTGTACGAACATGGGACGCTG 480
DB 469 CGCATCAITTCACAGGATATGAAGCCTGCAATATTTTACTTGTACGAACATGGGACGCTG 528
QY 481 CACATCACAGATTTCAACATTTCTGCGATGCTGCCAGGGAGACACAGATTACCAACCATG 540
DB 529 CACATCACAGATTTCAACATTTCTGCGATGCTGCCAGGGAGATACAGATTACCAACCATG 588
QY 541 GCTGGCACCAGCCTTACATGACCTGAGATGTTTTCAGCTCCAGAAAAGGAGCAGGCTAT 600
DB 589 GCTGGCACCAGCCTTACATGACCTGAGATGTTTTCAGCTCCAGAAAAGGAGCAGGCTAT 648
QY 601 TCTTTGCTGTGACTGCTGGTGGTCCCTGGGAGTGACGGATATGAAGTCTGAGAGCGCG 660
DB 649 TCTTTGCTGTGACTGCTGGTGGTCCCTGGGAGTGACGGATATGAAGTCTGAGAGCGCG 708
QY 661 AGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAAATGTTACACACAGTTCGAGAG 720
DB 709 AGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAAATGTTACACACAGTTCGAGAG 768
QY 721 ACTGTTGTAACCTTACCTTCTGCTGCTGACAGGAAATGTTTCACTTCTTAAAAGCTA 780
DB 769 ACTGTTGTAACCTTACCTTCTGCTGCTGACAGGAAATGTTTCACTTCTTAAAAGCTA 828
QY 781 CTCGAACCTTAATCCAGACCAACAGATTTTCTCAGTTATCTGATGTCCAGAACTTCCCGTAT 840
DB 829 CTCGAACCTTAATCCAGACCAACAGATTTTCTCAGTTATCTGATGTCCAGAACTTCCCGTAT 888
QY 841 ATGAATGATATAAATCGGATGCTGCTTTTTCAGAGAGGCTCATTCAGAGTTTCATTCCT 900
DB 889 ATGAATGATATAAATCGGATGCTGCTTTTTCAGAGAGGCTCATTCAGAGTTTCATTCCT 948
QY 901 AATAAGGAGGCTGAATGTGATCCTTCTGAACTTTGAGGAAATGATTTTGGAGTCC 960
DB 949 AATAAGGAGGCTGAATGTGATCCTTCTGAACTTTGAGGAAATGATTTTGGAGTCC 1008
QY 961 AAACCTCTACATAAGAAAAAAGGCTCTGGCAAGAGAGGAGATATCAGGAATGC 1020
DB 1009 AAACCTCTACATAAGAAAAAAGGCTCTGGCAAGAGAGGAGATATCAGGAATGC 1068
QY 1021 GATTCCTCTCAGACATGCTTCTTCAAGAGACCTTGATCTGTCCAGAGAGGATTCATA 1080
DB 1069 GATTCCTCTCAGACATGCTTCTTCAAGAGACCTTGATCTGTCCAGAGAGGATTCATA 1128
QY 1081 ATTTTCAACAGAGAAAAAGTAAACAGGACTTTTAAACAAAGACACCAAAATCTAGCCTTG 1140
DB 1129 ATTTTCAACAGAGAAAAAGTAAACAGGACTTTTAAACAAAGACACCAAAATCTAGCCTTG 1188
QY 1141 GAACAAACAAAGACCCCAAGTGACAAATGGACAAATGGACA 1183
DB 1189 GAACAAACAAAGACCCCAAGGTGAGGATGTCAGATAACA 1231
```

RESULT 9

ACA62840.
ID ACA62840 standard; cDNA; 1485 BP.

XX AC ACA62840;

DT 01-SEP-2003 (first entry)

XX cDNA encoding human kinase.

KW Human; ss: gene; kinase; gene therapy; cancer; inflammation; psoriasis;
arteriosclerosis.

OS Homo sapiens.

Key Location/Qualifiers

5'UTR 1..2

FT /*tag= a

FT 3..1193

FT /*tag= b

FT 3'UTR /product= "Kinase"
1194..1475
/*tag= C

XX US2003027307-A1.

XX 06-FEB-2003.

XX 26-SEP-2002; 2002US-00254869.

XX 09-MAR-2001; 2001US-00801876.

XX (APPL-) APPLERA CORP.

XX Ye J, Yan C, Di Francesco V, Beasley EM;

XX WPI; 2003-492035/58.

XX P-PSDB; ABU62276.

XX New isolated human kinase proteins, useful for treating disorders
mediated by kinase pathway (e.g. cancers, inflammations, arteriosclerosis
or psoriasis), or for development of human therapeutics and diagnostic
compositions.

XX Claim 4; Fig 1; 185pp; English.

XX The invention relates to a new isolated human kinase peptide. The human
kinase peptide and nucleic acid molecules are useful in the development
of human therapeutics and diagnostic compositions. The peptides are
useful for treating disorders (e.g. cancers, inflammations,
arteriosclerosis or psoriasis) characterised by an absence of,
inappropriate, or unwanted expression of the kinase protein. These
molecules are particularly useful as models for developing human
therapeutic targets, identifying therapeutic proteins, or serving as
targets for the development of human therapeutic agents that modulate
kinase activity in cells and tissues that express the kinase. The
peptides are also useful for raising antibodies or eliciting an immune
response; as a reagent (including the labelled reagent) in assays
designed to quantitatively determine levels of the protein (or its
binding partner or ligand) in biological fluids; or as markers for
tissues in which the corresponding protein is preferentially expressed.
The agents identified are useful for treating a subject with a disorder
mediated by kinase pathway. The present sequence represents cDNA encoding
a human kinase

XX Sequence 1485 BP; 471 A; 316 C; 331 G; 367 T; 0 U; 0 Other;

Query Match 94.8%; Score 1160.6; DB 9; Length 1485;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 1169; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

```
QY 1 ATGGAGCCCAACTTCAAGAAACCAACCAAGTGTGATGAAATGAAGATGTCACATTT 60
DB 3 ATGGAGCCCAACTTCAAGAAACCAACCAAGTGTGATGAAATGAAGATGTCACATTT 62
QY 61 GACCACCTTCAAAATTTTGGAGCCATTGGAAAGGCGAGTTTTCGGAAGGCTCTCATTTGA 120
DB 63 GACCACCTTCAAAATTTTGGAGCCATTGGAAAGGCGAGTTTTCGGAAGGCTCTCATTTGA 122
QY 121 CAGAAGAAATGATACCAAGAGATGTAGCAATCAAGTACATGATAAACAAGAGTGGTG 180
DB 123 CAGAGAAATGATACCAAGAGATGTAGCAATCAAGTACATGATAAACAAGAGTGGTG 182
QY 181 GAGCGCAATGAAGTGAGAAATGCTTCCAGGAATCTCCAGATCATGAGGCTCTGGAGCAC 240
DB 183 GAGCGCAATGAAGTGAGAAATGCTTCCAGGAATCTCCAGATCATGAGGCTCTGGAGCAC 242
QY 241 CTTTCTCTGGTTAAATTTGTGTTATCTCTCAAGATGAGGAACACATGTTTCATGGTGGTG 300
DB 243 CTTTCTCTGGTTAAATTTGTGTTATCTCTCAAGATGAGGAACACATGTTTCATGGTGGTG 302
QY 301 GACCTCTCTGGTGGAGACCTCGGTTATCACCTGCAACAGAACGTCCACTTCAAGGAA 360
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XX Homo sapiens.

Claim 4: Fig 1: 174pp: English.

XX
SQ Sequence 1485 BP; 471 A; 316 C; 331 G; 367 T; 0 U; 0 Other;

Query Match 94.8%; Score 1160.6; DB 10; Length 1485;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 1169; Conservative 0; Mismatches 14; Indels 0;

```
QY 1 ATGGGAGCCCAACACCTTCAAGAAACACCAAGGAGTGTGATGAAATCAAGATGCAACTTT 60
Db 3 ATGGGAGCCCAACACCTTCAAGAAACACCAAGGAGTGTGATGAAATCAAGATGCAACTTT 62
QY 61 GACCACTTTGAAATTTTGGAGCCATTTGGGAAAGGAGTGTGGAAGAGTCTGCAATGTA 120
Db 63 GACCACTTTGAAATTTTGGAGCCATTTGGGAAAGGAGTGTGGAAGAGTCTGCAATGTA 122
QY 121 CAGAAGATGATACCAAGAGATGTACGCAATGCAAGTACATCAATAAACAAAGTGCCTG 180
Db 123 CAGAAGATGATACCAAGAGATGTGCGCAATGCAAGTACATCAATAAACAAAGTGCCTG 182
QY 181 GAGCGCAATGAGTGAAGAAATGCTTCAAGAACTCCAGATCATGCGAGTCTGGAGCAC 240
Db 183 GAGCGCAATGAGTGAAGAAATGCTTCAAGAACTCCAGATCATGCGAGTCTGGAGCAC 242
QY 241 CCTTTCCCTGGTTAAATTTGGTGTATTCCTTCCAAAGATGAGGAAGACATGTTCTGTTG 300
Db 243 CCTTTCCCTGGTTAAATTTGGTGTATTCCTTCCAAAGATGAGGAAGACATGTTCTGTTG 302
QY 301 GACCTCCTGCTGGTGGAGACCTGCGTTATCACTGCAACAGACGTCCTCAAGGAA 360
Db 303 GACCTCCTGCTGGTGGAGACCTGCGTTATCACTGCAACAGACGTCCTCAAGGAA 362
QY 361 GAAACAGTGAAGCTCTTCAATCTGTGAGTGTGTCATGGCCCTGAGTACTGCGAGAAC 420
Db 363 GAAACAGTGAAGCTCTTCAATCTGTGAGTGTGTCATGGCCCTGAGTACTGCGAGAAC 422
QY 421 CSCATCATTCACAGGATGATGAAGCTGACATATTTTACTTGACGAACATGGGACCTG 480
Db 423 CSCATCATTCACAGGATGATGAAGCTGACATATTTTACTTGACGAACATGGGACCTG 482
QY 481 CACATCACAGATTTCAACATTCCTGCGATGCTGCCAGGAGACACAGATTACCAACATG 540
Db 483 CACATCACAGATTTCAACATTCCTGCGATGCTGCCAGGAGACACAGATTACCAACATG 542
QY 541 GCTGSCCAACGCTTACATGSCACCTGAGATGTTTCACTCCAGAAAAGGAGGAGCTAT 600
Db 543 GCTGSCCAACGCTTACATGSCACCTGAGATGTTTCACTCCAGAAAAGGAGGAGCTAT 602
QY 601 TCTTTTGTCTGTGATGCTGTGCTGCTGCGAGTACGCGATATGAACTCTCAGAGGCCGG 660
Db 603 TCTTTTGTCTGTGATGCTGTGCTGCGAGTACGCGATATGAACTCTCAGAGGCCGG 662
QY 661 AGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAAATTTGACACACGTTTGAGACG 720
Db 663 AGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAAATTTGACACACGTTTGAGACG 722
QY 721 ACTGTTGTAACTTACCTCTCTGCTGCTGCTGCAAGGAAATGGTGTCACTTCTTAAAGCTA 780
Db 723 ACTGTTGTAACTTACCTCTCTGCTGCTGCTGCAAGGAAATGGTGTCACTTCTTAAAGCTA 782
QY 781 CTCGAACCTAATCCAGACCAACGATTTTCTCAGTTATCTGATGTCAGAACTTCCCGTAT 840
Db 783 CTCGAACCTAATCCAGACCAACGATTTTCTCAGTTATCTGATGTCAGAACTTCCCGTAT 842
QY 841 ATGAATGATATAAATCTGGATGCAAGTTTTCAGAAAGGCTCATTCAGGTTTCATTCCT 900
Db 843 ATGAATGATATAAATCTGGATGCAAGTTTTCAGAAAGGCTCATTCAGGTTTCATTCCT 902
QY 901 AATAAGCAGCGCTGAATTTGTGATCCTACCTTTCGAACTTGAGGAATGATTTTCGAGTCC 960
Db 903 AATAAGCAGCGCTGAATTTGTGATCCTACCTTTCGAACTTGAGGAATGATTTTCGAGTCC 962
QY 961 AAACCTCTACATAAGAAAAAAGCGTCTGGCAAGAGGAGAGGATATGAGGAATGC 1020
Db 963 AAACCTCTACATAAGAAAAAAGCGTCTGGCAAGAGGAGAGGATATGAGGAATGC 1022
QY 1021 GATCTCTCTCAGACATGCTTCTTCAAGAGCACCTTGACTCTGTCCAGAGAGGATTCATA 1080
Db 1023 GATCTCTCTCAGACATGCTTCTTCAAGAGCACCTTGACTCTGTCCAGAGAGGATTCATA 1082
QY 1081 ATTTTCAACAGAGAAAAAGTAAACAGGAGCTTTTAAACAAAGACACCAAAATCTAGCCTTG 1140
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Db 1083 ATTTTCAACAGAGAAAAAGTAAACAGGAGCTTTTAAACAAAGACACCAAAATCTAGCCTTG 1142
QY 1141 GAACAAACCAAGACCCACAAAGTACAAATGACAAATGGACAAATGGACA 1183
Db 1143 GAACAAACCAAGACCCACAAAGTACAAATGACAAATGGATGTCAGAAATACA 1185

RESULT 11
ADL09161
ID ADL09161 standard; cDNA; 1485 BP.
XX AC ADL09161;
XX DT 20-MAY-2004 (first entry)
XX Human protein kinase, cDNA.
XX gene; ss; human; Kinase Modulator;
XX serine/threonine protein kinase subfamily; Gene Therapy; protein kinase.
XX Homo sapiens.
XX Key Location/Qualifiers
XX CDS 3..1193
XX FT /*tag= a
XX FT /product= "Human protein kinase"
XX US2004043466-A1.
XX PD 04-MAR-2004.
XX PF 23-SEP-2003; 2003US-00667442.
XX PR 09-MAR-2001; 2001US-00801876.
XX PR 26-SEP-2002; 2002US-00254869.
XX PA (APPL-) APPLERA CORP.
XX PI Ye J, Yan C, Di Francesco V, Beasley EM;
XX WPI; 2004-280746/26.
XX DR P-PSDB; ADL09162.
XX New isolated human kinase peptides, useful as models for developing human
therapeutic targets, aid in the identification of therapeutic proteins,
or for diagnosing, preventing and treating kinase-related conditions.
XX Claim 4; SEQ ID NO 1; 184pp; English.
XX The invention relates to new isolated human protein kinase polypeptide
and polynucleotides. The new human kinase protein is related to the
serine/threonine protein kinase subfamily. The kinase peptides and
nucleic acid molecules are useful as models for the development of human
therapeutic targets, aid in the identification of therapeutic proteins,
and serve as targets for the development of human therapeutic agents that
modulate kinase activity in cells and tissues that express the kinase.
The peptides are also useful in the diagnosis, prevention and treatment
of kinase-related conditions. The peptide may be used in drug screening
assays, in assays to determine the biological activity of the protein, to
raise antibodies or to elicit another immune response, as a reagent in
assays designed to quantitatively determine levels of the protein in
biological fluids, or as markers for tissues in which the corresponding
protein is preferentially expressed. The antibodies are useful in
pharmacogenomic analysis, for inhibiting protein function, or for tissue
typing. The nucleic acid molecules are useful as probes, primers,
chemical intermediates, or in biological assays. The present sequence
represents the cDNA encoding the human protein kinase.
XX Sequence 1485 BP; 471 A; 316 C; 331 G; 367 T; 0 U; 0 Other;
Query Match 94.8%; Score 1160.6; DB 12; Length 1485;
Best Local Similarity 98.8%; Pred. No. 0;
```

Matches 1169; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 1 ATGGAGCAACACTTCAAGAAAACCAACAGTGTGTTGATGAATAATGAAGATGTCAACTTT 60
Db 3 ATGGAGCAACACTTCAAGAAAACCAACAGTGTGTTGATGAATAATGAAGATGTCAACTTT 62

Qy 61 GACCACCTTTGAAATTTTTCGAGCCATTGGGAAAGCGAGTTTGGGAAAGTCTGCATTGTA 120
Db 63 GACCACCTTTGAAATTTTTCGAGCCATTGGGAAAGCGAGTTTGGGAAAGTCTGCATTGTA 122

Qy 121 CAGAAGATGATACCAAGAAGATGACCAATGAAGTACATGAATAAACAAGTGGGTG 180
Db 123 CAGAAGATGATACCAAGAAGATGACCAATGAAGTACATGAATAAACAAGTGGGTG 182

Qy 181 GAGCGCAATGAGTGAAGATGCTTCAAGAACTCCAGATCATGCGGGTCTGGAGCAC 240
Db 183 GAGCGCAATGAGTGAAGATGCTTCAAGAACTCCAGATCATGCGGGTCTGGAGCAC 242

Qy 241 CCTTTCTGCTGTTAATTTGTGTTATTCCTTCCAAGATGAGGAAGACATGTTTCATGTTG 300
Db 243 CCTTTCTGCTGTTAATTTGTGTTATTCCTTCCAAGATGAGGAAGACATGTTTCATGTTG 302

Qy 301 GACCTCTGCTGCTGGTGGAGACTCGCTTATCACCTGCAACAGACGCTCCACTTCAAGGAA 360
Db 303 GACCTCTGCTGCTGGTGGAGACTCGCTTATCACCTGCAACAGACGCTCCACTTCAAGGAA 362

Qy 361 GAAACAGTGAAGCTTCACTGTGAGTGTGTCATGCGCCCTGGACTACCTGCGAAGCAG 420
Db 363 GAAACAGTGAAGCTTCACTGTGAGTGTGTCATGCGCCCTGGACTACCTGCGAAGCAG 422

Qy 421 CGCATCTTCAACAGGATATGAAGCTGACAAATTTTACTTGACGACATGCGGACGCTG 480
Db 423 CGCATCTTCAACAGGATATGAAGCTGACAAATTTTACTTGACGACATGCGGACGCTG 482

Qy 481 CACATCAAGATTTCAACATTTGCTGCGATGCTGCCAGGAGACACAGATTTACCACCATG 540
Db 483 CACATCAAGATTTCAACATTTGCTGCGATGCTGCCAGGAGACACAGATTTACCACCATG 542

Qy 541 GCTGGCCACCAAGCTTATAGGCACTGAGATGTTTCACTCCAGAAAGGAGCAGGCTAT 600
Db 543 GCTGGCCACCAAGCTTATAGGCACTGAGATGTTTCACTCCAGAAAGGAGCAGGCTAT 602

Qy 601 TCCCTTCTGTTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
Db 603 TCCCTTCTGTTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 662

Qy 661 AGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAAATTTGACACACGTTTGAGACG 720
Db 663 AGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAAATTTGACACACGTTTGAGACG 722

Qy 721 ACTGTTGTAACCTTACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
Db 723 ACTGTTGTAACCTTACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 782

Qy 781 CTGCAACTAATCAGACCAACGATTTCTCAGTATCTGATGTCAGAACTTCCCGTAT 840
Db 783 CTGCAACTAATCAGACCAACGATTTCTCAGTATCTGATGTCAGAACTTCCCGTAT 842

Qy 841 ATGAATGATATAAATCGGATGCGAGTTTTCAGAAAGGCTCATTTCCAGGTTTCATTCCT 900
Db 843 ATGAATGATATAAATCGGATGCGAGTTTTCAGAAAGGCTCATTTCCAGGTTTCATTCCT 902

Qy 901 AATAAGGCGAGGCTGAATTTGATCTTCACTTCTGAGTGAAGTGAATTTGGAGTCC 960
Db 903 AATAAGGCGAGGCTGAATTTGATCTTCACTTCTGAGTGAAGTGAATTTGGAGTCC 962

Qy 961 AAACCTTACATAGAAAAAAGGCTTGCAGAAAGGAGGAGATATGAGGAATGC 1020
Db 963 AAACCTTACATAGAAAAAAGGCTTGCAGAAAGGAGGAGATATGAGGAATGC 1022

Qy 1021 GATTCCTTCTCAGACATGCTTCTTCAAGAGCACCTTGCATCTGTCAGAAAGGAGTTCATA 1080
Db 1023 GATTCCTTCTCAGACATGCTTCTTCAAGAGCACCTTGCATCTGTCAGAAAGGAGTTCATA 1082

Qy 1081 ATTTTCAACAGAGAAAAGTAAACAGGACTTTTAAACAAAAGACAAACCAATCTAGCCTTG 1140
Db 1083 ATTTTCAACAGAGAAAAGTAAACAGGACTTTTAAACAAAAGACAAACCAATCTAGCCTTG 1142

Qy 1141 GAACAAACCAAGAACCCACCAAGTGCACAAATGGACAAATGGACA 1183
Db 1143 GAACAAACCAAGAACCCACCAAGTGCACAAATGGACAAATGGACA 1185

RESULT 12
ADM01546
ID ADM01546 standard; cDNA; 2063 BP.
XX
AC ADM01546;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human cDNA of the invention SEQ ID NO:231.
XX
KW ss; gene; human; gene therapy; diagnostic marker; pharmaceutical.
XX
OS Homo sapiens.
XX
PN EPI347046-A1.
XX
PD 24-SEP-2003.
XX
PF 12-APR-2002; 2002EP-00008400.
XX
PR 22-MAR-2002; 2002JP-00137785.
XX
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
XX
DR WPI; 2003-723558/69.
DR P-PSDB; ADM03989.
XX
PT New polynucleotides and polypeptides are useful in gene therapy, for
PT developing a diagnostic marker or medicines for regulating their
PT expression and activity, or as a target of gene therapy.
XX
PS Claim 1; SEQ ID NO 231; 305pp; English.
XX
CC The invention relates to a novel human polynucleotide and the encoded
CC polypeptide. A polynucleotide of the invention may have a use in gene
CC therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful
CC as a primer for synthesizing the polynucleotide or as a probe for
CC detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are
CC useful in gene therapy, for developing a diagnostic marker or medicines
CC for regulating their expression and activity, or as a target of gene
CC therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides
CC are useful as pharmaceutical agents. The present sequence represents a
CC cDNA sequence of the invention.
XX
SQ Sequence 2063 BP; 556 A; 463 C; 500 G; 544 T; 0 U; 0 Other;

Query Match 84.3%; Score 1032.2; DB 11; Length 2063;
Best Local Similarity 99.7%; Pred. No. 4e-290;
Matches 1034; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ATGGAGCCCAACACTTCAAGAAAACCAACAGTGTGTTGATGAATAATGAAGATGTCAACTTT 60
Db 334 ATGGAGCCCAACACTTCAAGAAAACCAACAGTGTGTTGATGAATAATGAAGATGTCAACTTT 393

Qy 61 GACCACCTTTGAAATTTTTCGAGCCATTGGGAAAGCGAGTTTGGGAAAGTCTGCATTGTA 120
Db 394 GACCACCTTTGAAATTTTTCGAGCCATTGGGAAAGCGAGTTTGGGAAAGTCTGCATTGTA 453

Qy 121 CAGAAGATGATACCAAGAAGATGTCAGCAATGAAGTACATGAATAAACAAGTGGGTG 180

QY 1 ATGGAGCCACACTTCAAGAAACACACAGTGTGTTGATGAAATGAGATGTCACCTTT 60
Db 252 ATGGAGCCACACTTCAAGAAACACACAGTGTGTTGATGAAATGAGATGTCACCTTT 311
QY 61 GACCACCTTTGAAATTTTGGAGCCATTGGGAAAGGAGTTTGGGAAAGTCTGCAATGTA 120
Db 312 GACCACCTTTGAAATTTTGGAGCCATTGGGAAAGGAGTTTGGGAAAGTCTGCAATGTA 371
QY 121 CAGAAGATGATACCAAGAGATGTACGCAATGAAGTACATGAATAAACAAAGTGGGTG 180
Db 372 CGGAAGATGATACCAAGAGATGTACGCAATGAAGTACATGAATAAACAAAGTGGGTG 431
QY 181 GAGCGCAATGAAGTGAAGATGTTTCAAGGATCTCCAGATCATGCGAGGTCTGGAGCAC 240
Db 432 GAGCGCAATGAAGTGAAGATGTTTCAAGGATCTCCAGATCATGCGAGGTCTGGAGCAC 491
QY 241 CCTTTCTCGTGAATTTGTTGTTGTTTCTTCAAGATGAGGAAGATGTTTCATGTTGGTG 300
Db 492 CCTTTCTCGTGAATTTGTTGTTGTTTCTTCAAGATGAGGAAGATGTTTCATGTTGGTG 551
QY 301 GACCTCTCTGTTGGTGGAGACCTGCGTTATCACTGCAACAGAACTGTCCTCAAGGAA 360
Db 552 GACCTCTCTGTTGGTGGAGACCTGCGTTATCACTGCAACAGAACTGTCCTCAAGGAA 611
QY 361 GAAACAGTGAAGCTCTTCACTGCTGAGCTGCTGATGCGCTGAGTACCTGCGAAGCCAG 420
Db 612 GAAACAGTGAAGCTCTTCACTGCTGAGCTGCGTATGCGCTGAGTACCTGCGAAGCCAG 671
QY 421 CGCATCATTCACAGGATATGAAGCTGACAAATATTTTACCTGACGAACATGGGACCGTG 480
Db 672 CGCATCATTCACAGGATATGAAGCTGACAAATATTTTACCTGACGAACATGGGACCGTG 731
QY 481 CACATCACAGATTTCAACTGCTGCGATGCTGCCAGGAGACACAGATTTACCAACATG 540
Db 732 CACATCACAGATTTCAACTGCTGCGATGCTGCCAGGAGACACAGATTTACCAACATG 791
QY 541 GCTGGCACCAAGCTTACATGCGACCTGAGATGTTTACGCTCCAGAAAGGACGCGTAT 600
Db 792 GCTGGCACCAAGCTTACATGCGACCTGAGATGTTTACGCTCCAGAAAGGACGCGTAT 851
QY 601 TCCTTTGCTGTTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
Db 852 TCCTTTGCTGTTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 911
QY 661 AGACCGTATCATATTCCTCCAGTCTCCAGTCTCCAGTCTCCAGTCTCCAGTCTCCAGT 720
Db 912 AGACCGTATCATATTCCTCCAGTCTCCAGTCTCCAGTCTCCAGTCTCCAGTCTCCAGT 971
QY 721 ACTGTTGTAATTAACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
Db 972 GCAATTGTAATTAACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1031
QY 781 CTCGAACCTAATCCAGAACCAAGATTTTCTCAGTTATCTGATGTCAGAACTTCCCGTAT 840
Db 1032 CTTGAACTAATCCAGAACCAAGATTTTCTCAGTTATCTGATGTCAGAACTTCCCGTAT 1091
QY 841 ATGAATGATATAACTGGGATGCAAGTTTTCAGAAAGGCTCAATTCAGGTTTCATTCCT 900
Db 1092 ATGAATGATATAACTGGGATGCAAGTTTTCAGAAAGGCTCAATTCAGGTTTCATTCCT 1151
QY 901 AATAAGGAGGCTGATTTGATCTTACCTTGAACCTTGAAGAAATGATTTGGAGTCC 960
Db 1152 ACCAAGGAGGCTGATTTGATCTTGAACCTTGAAGAAATGATTTGGAGTCC 1211
QY 961 AAACCTCTACATAGAAAAAAGCGTCTGCAAGAGGAGGAGGATATGAGAAATGC 1020
Db 1212 AAACCTCTACATAGAAAAAAGCGTCTGCAAGAGGAGGAGGATATGAGAAATGC 1271
QY 1021 GATTCCTCTCAGACATGCTTCTTCAAGAGCACCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
Db 1272 GATTCCTCTCAGACATGCTTCTTCAAGAGCACCTGCTGCTGCTGCTGCTGCTGCTGCTG 1331
QY 1081 ATTTTCAACAGAAAAAGTAAACAGGACCTTTTAAACAAAGACAAACCAATCTAGCCTTG 1140

Db 1332 ATTTTCAACAGAAAAAGTAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1391
QY 1141 GAACAAACCAAGAC 1155
Db 1392 GAACAAACCAAGAC 1406
RESULT 14
ADP44497
ID ADP44497 standard; cDNA; 3766 BP.
XX
AC ADP44497;
XX AC
XX DT 12-FEB-2004 (first entry)
XX Mouse kinase protein encoding cDNA SEQ ID NO:15.
XX cytostatic; nootropic; neuroprotective; antidiabetic; screening;
XX regulation; drug development; protein-associated disease; cancer;
XX dementia; diabetes; kinase; enzyme; mouse; gene; ss.
XX Mus musculus.
XX WO2003084992-A1.
XX 16-OCT-2003.
XX 04-APR-2003; 2003WO-JP004330.
XX 05-APR-2002; 2002JP-00103396.
XX 23-APR-2002; 2002JP-00120904.
XX 02-MAY-2002; 2002JP-00130601.
XX 04-DEC-2002; 2002JP-00352520.
XX (RIKE) RIKEN KK.
XX (DNAP-) DNAFORM KK.
XX (MITU) MITSUBISHI CHEM CORP.
XX Hayashizaki Y, Kamiya M, Kubodera H, Watanabe W;
XX WPI; 2003-833568/77.
XX P-PSDB; ADP44523.
XX
XX Proteins and encoded DNAs with kinase activity, useful in screening
XX substrates for regulating such activity and in developing drugs for the
XX protein-associated diseases e.g. cancer, dementia and diabetes.
XX
XX Claim 4; SEQ ID NO 15; 342pp; Japanese.
XX
XX The present invention describes a protein: (a) containing any of the
XX amino acid sequences of ADP44509 to ADP44534 or ADP44544; or (b) based on
XX any of the sequences in (a) but with some amino acids deleted,
XX substituted and/or added and having kinase activity. Also described: (1)
XX a DNA encoding any of the proteins; (2) a full-length cDNA encoding the
XX protein; (3) a DNA which is: (a) a DNA containing any of the base
XX sequences in ADP44483 to ADP44508 or ADP44543; (b) a DNA derived from any
XX of the sequences in (a) but with some bases deleted, substituted and/or
XX added and encoding a protein with kinase activity; or (c) a DNA
XX hybridisable with any of the sequences in (a) or their complementary
XX strands under stringent conditions and encoding a protein with kinase
XX activity; (4) a recombinant vector containing the DNA; (5) a cell
XX transfected with the DNA or recombinant vector, or an individual produced
XX from the cell; (6) recombinant proteins produced by such cells; (7) an
XX oligonucleotide containing 5-10 consecutive bases in any of the base
XX sequences, its sense oligonucleotide, an antisense oligonucleotide with a
XX complementary strand of such sense oligonucleotide; (8) an antibody
XX derivative of the (anti-)sense oligonucleotide; (9) a method for
XX specifically binding to the protein, or its partial fragment; (9) a
XX method for screening substances for regulating activity of the protein by
XX contacting a test substance with such protein before measuring changes in
XX the protein activity due to the test substance; (10) a method for
XX screening substances regulating expression of the DNA by contacting a

CC disorders (e.g. schizophrenia), neurodegenerative disorders (e.g.
CC Parkinson's disease), inflammatory disorders (e.g. asthma), infectious
CC disease (e.g. HIV) and reproductive disorders (e.g. infertility).
CC Additionally, polynucleotides encoding protein kinases may be used for
CC gene therapy and as DNA probes in diagnostic assays. The protein kinase
CC polypeptides may be used as antigens in the production of antibodies
CC against the protein kinases and in assays to identify modulators of
CC protein kinase expression and activity
XX
SQ Sequence 981 BP; 294 A; 207 C; 245 G; 235 T; 0 U; 0 Other;

Query Match 68.0%; Score 832.8; DB 4; Length 981;
Best Local Similarity 90.8%; Pred. No. 4.3e-232;
Matches 904; Conservative 0; Mismatches 77; Indels 15; Gaps 1;

Qy 1 ATGGGAGCCAACTTCAAGAAAAACCCAGTGTGTTGATGAAATGAAGATGTCAACTTT 60
Db 1 ATGGGAGCCAACTTCAAGAAAAACCCAGTGTGTTGATGAAATGAAGATGTCAACTTT 60

Qy 61 GACCACTTGGAAATTTGCGAGCCATTGGGAAGGCGAGTTTGGGAAGGCTCGCATTTGA 120
Db 61 GACCACTTGGAAATTTGCGAGCCATTGGGAAGGCGAGTTTGGGAAGGCTCGCATTTGA 120

Qy 121 CAGAAGAAATGATACCAAGAAAGATGTAGCAATGAAGTACATGAATAACAAAAGTGGGTG 180
Db 121 CAGAAGAAATGATACCAAGAAAGATGTAGCAATGAAGTACATGAATAACAAAAGTGGGTG 180

Qy 181 GAGCGCAATGAAGTGAAGAAATGTCTTCAAGAACTCCAGATCATGCGGGTCTGGAGCAC 240
Db 181 GAGCGCAATGAAGTGAAGAAATGTCTTCAAGAACTCCAGATCATGCGGGTCTGGAGCAC 240

Qy 241 CTTTCTCTGTTAATTTGTTGGTATTTCTTCAAGATGAGGAAGACATGTTTCATGTTGGTG 300
Db 241 CTTTCTCTGTTAATTTGTTGGTATTTCTTCAAGATGAGGAAGACATGTTTCATGTTGGTG 300

Qy 301 GACCTCTCTGCTGGGTGGAGACTCGCTTATCACCTGCAACAGAACCTCCACTTCAAGGAA 360
Db 301 GACCTCTCTGCTGGGTGGAGACTCGCTTATCACCTGCAACAGAACCTCCACTTCAAGGAA 360

Qy 361 GAAACAGTGAAGCTCTTTCATCTGTGAGCTGTGTCATGCGCTGATGCGCTGGAGTACCTG 420
Db 361 GAAACAGTGAAGCTCTTTCATCTGTGAGCTGTGTCATGCGCTGATGCGCTGGAGTACCTG 420

Qy 421 CGCATCATTCACAGGATATGAAGCTGACATATTTTACTTTGACGAACATGCGGCACGTG 480
Db 421 CGCATCATTCACAGGATATGAAGCTGACATATTTTACTTTGACGAACATGCGGCACGTG 480

Qy 481 CACATCAGATTTTCAACATTTGCTGCGATGCTGCCAGGAGACACAGATTACCACCATG 540
Db 481 CACATCAGATTTTCAACATTTGCTGCGATGCTGCCAGGAGACACAGATTACCACCATG 540

Qy 541 GCTGGCACCAAGCCTTACATGGCACCTGAGATGTTTCAGCTCCAGAAAAGGAGCAGGCTAT 600
Db 541 GCTGGCACCAAGCCTTACATGGCACCTGAGATGTTTCAGCTCCAGAAAAGGAGCAGGCTAT 600

Qy 601 TCCTTTGCTGTGATGCTGCTGCTGGAGTGAAGGATGATGAACTGCTGAGAGGCGGG 660
Db 601 TCCTTTGCTGTGATGCTGCTGCTGGAGTGAAGGATGATGAACTGCTGAGAGGCGGG 660

Qy 661 AGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAATTTGTACACACGTTTGAGACG 720
Db 661 AGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAATTTGTACACACGTTTGAGACG 720

Qy 721 ACTGTTGTAACTTACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
Db 721 ACTGTTGTAACTTACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780

Qy 781 CTCGAACTTAATCAGACCAACAGATTTTCTCAGTTATCTGATGTCAGAACTTCCCGTAT 840
Db 781 AGAAGGAAGACTGCATGTC-----CAACCGAAGTAACAAAAGGAAGCAGG 825

Qy 841 ATGAATGATATAAAGTGGATGCGAGTTTTCAGAGAGGCTCATTTCCAGGTTTTCATTCCT 900

Db 826 CTCTCTGGCTTAACTTTAGTAAGTTTAGTATACAAATATTGGGACACCAACTCTCTTCTTG 885
Qy 901 AATRAAGGCGAGGCTGAATTTGTGATCCTACCTTTGAACTTGAGGAATGAATTTGGAGTCC 960
Db 886 CAGAAAGGCGAGGCTGAATTTGTGATCCTACCTTTGAACTTGAGGAATGAATTTGGAGTCC 945
Qy 961 AAACCTCTACATAAGAAAAAAGCGTCTGCAAG 996
Db 946 AAACCTCTACATAAGAAAAAAGCGTCTGCAAG 981

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Job time : 473 secs

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OM nucleic - nucleic search, using sw model

Run on: December 20, 2004, 02:05:31 ; Search time 3705 Seconds
(without alignments)
15622.832 Million cell updates/sec

Title: US-10-620-845-8
Perfect score: 1224
Sequence: 1 atgggagccacacttcaag.....agacctggaagtttataa 1224

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*
1: gb_ba.*
2: gb_hcg.*
3: gb_in.*
4: gb_on.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pi.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1224	100.0	1224	6	AR393902 Sequence
2	1224	100.0	1224	6	AX303183 Sequence
3	1224	100.0	1675	6	AR393904 Sequence
4	1224	100.0	1675	6	AX303187 Sequence
5	1165.4	95.2	1191	6	AR393903 Sequence
6	1165.4	95.2	1191	6	AX303185 Sequence
7	1165.4	95.2	1594	6	AX207388 Sequence
8	1165.4	95.2	1594	6	AX766348 Sequence
9	1163.8	95.1	1191	6	AX320936 Sequence
10	1163.8	95.1	1281	6	AX320934 Sequence
11	1160.6	94.8	1485	6	AR265353 Sequence
12	1160.6	94.8	1485	6	AR432044 Sequence
13	1032.2	84.3	2063	6	AX833107 Sequence
14	1032.2	84.3	2063	9	AK094580 Homo sapi
15	832.8	68.0	981	6	AX166513 Sequence
16	773	63.2	4973	10	BC055002 Mus muscu
17	726.4	59.3	2229	5	BX950341 Gallus ga
18	661	54.0	711	6	AR393901 Sequence
19	661	54.0	711	6	AX303181 Sequence

20	660	53.9	678	6	AR393900	AR393900 Sequence
21	660	53.9	678	6	AX303179	AX303179 Sequence
22	628.2	51.3	1456	5	BC072876	BC072876 Xenopus l
23	558.4	45.6	3367	10	BC052404	BC052404 Mus muscu
24	558.4	45.6	3367	10	BC058412	BC058412 Mus muscu
25	558.4	45.6	3449	10	BC056396	BC056396 Mus muscu
26	555.2	45.4	2045	10	MMU250840	AJ250840 Mus muscu
27	542.4	44.3	3224	6	AX056360	AX056360 Sequence
28	542.4	44.3	3224	9	HSA250839	AX250839 Homo sapi
29	540.8	44.2	3236	9	BC038238	BC038238 Homo sapi
30	519.6	42.5	3244	6	AX376504	AX376504 Sequence
31	519.6	42.5	3244	9	AY358353	AY358353 Homo sapi
32	497.6	40.7	2184	10	BC026457	BC026457 Mus muscu
33	497.6	40.7	2201	10	AB041542	AB041542 Mus muscu
34	484.8	39.6	1257	6	AR411704	AR411704 Sequence
35	484.8	39.6	1826	6	AR411703	AR411703 Sequence
36	484.8	39.6	2143	9	AY098866	AY098866 Homo sapi
37	483.2	39.5	1487	6	AX504245	AX504245 Sequence
38	483.2	39.5	1858	9	BC015792	BC015792 Homo sapi
39	479.4	39.2	1787	6	AX056359	AX056359 Sequence
40	476.4	38.9	2029	9	BC069203	BC069203 Homo sapi
41	472.4	38.6	827	9	BC021666	BC021666 Homo sapi
42	471.6	38.5	2028	9	BC045760	BC045760 Homo sapi
43	470	38.4	1864	6	AR456183	AR456183 Sequence
44	470	38.4	1864	6	AX642304	AX642304 Sequence
45	465.2	38.0	1591	6	AX768900	AX768900 Sequence

ALIGNMENTS

RESULT 1
AR393902
LOCUS AR393902 1224 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 8 from patent US 6617147.
ACCESSION AR393902
VERSION AR393902.1 GI:40121077
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1224)
AUTHORS Hu, Y., Nepomnichy, B., Wang, X. and Donoho, G.
TITLE Human kinase proteins and polynucleotides encoding the same
JOURNAL Patent: US 6617147-A 8 09-SEP-2003;
FEATURES
source
1. .1224
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN	Query Match	100.0%	Score 1224;	DB 6;	Length 1224;
	Best Local Similarity	100.0%;	Pred. No. 8.2e-311;		
	Matches 1224;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	ATGGAGCCCAACTTCAAGAAACCCACAGTGTGTTGATGAATAATGAAGATGTCAACTTT	60		
Db	1	ATGGAGCCCAACTTCAAGAAACCCACAGTGTGTTGATGAATAATGAAGATGTCAACTTT	60		
Qy	61	GACCACCTTGAATTTTGGAGCCATTTGGGAAAGGAGTTTGGGAGGTTCTGCATCTGA	120		
Db	61	GACCACCTTGAATTTTGGAGCCATTTGGGAAAGGAGTTTGGGAGGTTCTGCATCTGA	120		
Qy	121	CAGAAGATGATCAAGAAAGATGTACGCAATGAAGTACATGAATAACAAAGTCGCTG	180		
Db	121	CAGAAGATGATCAAGAAAGATGTACGCAATGAAGTACATGAATAACAAAGTCGCTG	180		
Qy	181	GAGCGCAATGAAGTGAATAATGTTCTTCAAGAACTCCAGATCATCGAGGTTCTGAGCAC	240		
Db	181	GAGCGCAATGAAGTGAATAATGTTCTTCAAGAACTCCAGATCATCGAGGTTCTGAGCAC	240		
Qy	241	CCTTTCTGTTAATTTTGGTATTTCTTCCAAGATGAGGAGACATGTTTCATGCTGGTG	300		

Db	241	CTTTCTCGTTAAATTTGTGGTATTCCTCCAAAGATGAGGAACATGTTTCATGTGGTG	300
Qy	301	GACCTCTGTGGTGGAGACCTGCGTTATCACTGCAACAGAACGTCACATTCAAAGGAA	360
Db	301		
Qy	361	GAACAGTGAAGCTCTTCATCTGTGAGCTGGTCAATGCCCCTGGACTACCTGCAAGAACCCAG	420
Db	361		
Qy	421	CGCATCAATCACAGGGATATGACCCCTGCAATAATTTTACTTCGACGAACATGGCCACGTG	480
Db	421		
Qy	481	CACATCACAGATTTCAACATTTGCTGCGATGTCGCCACGGAGACACAGATTCACCAATG	540
Db	481		
Qy	541	GCTGGACCAAGCCCTTACATGGCACTTGAGATGTTTCAGCTTCAGAAAGAGAGCAGGTAT	600
Db	541		
Qy	601	TCCTTTCTGTTGACTGCTGCTCCCTGGAGTGAAGCCATATGAATGCTGACAGGCCGG	660
Db	601		
Qy	661	AGACCGTATCATATTCGCTCCAGTACTTCAGCAAGGAAATGTGACACAGTTTGAGACG	720
Db	661		
Qy	721	ACTGTTGTAACTTACCTTCTGCCGTGTGTCACAGAAATGTTGTCACTTCTTAAAAAGCTA	780
Db	721		
Qy	781	CTCGAACTTAATCCAGACCAACGATTTTCTCAGTTATCTGATGTCCAGAACTTCCCGTAT	840
Db	781		
Qy	841	ATGAATGATATAAATCGGATGCAAGGAGGCTCAATCCAGGTTTCATTCCT	900
Db	841		
Qy	901	AATAAGGCAGGCTGAATTTGTGATCCTTACCTTTGAACTTGAGGAATGATTTTGGAGTCC	960
Db	901		
Qy	961	AAACCTCTACATAAGAAAAAAGCGCTGCGCAAGAGGAGGATATGAGGAATGC	1020
Db	961		
Qy	1021	GATTCCTTCAGACATGCTCTTTCAAGAGCACTTCGATCTGTCCAGAAAGGAGTTCAATA	1080
Db	1021		
Qy	1081	ATTTTCAACAGAAAAAGTTAAACAGGGACTTTTAAACAAAAAGCAACCAATCTAGCCTTG	1140
Db	1081		
Qy	1141	GAAACAAACCAAGCCACAGTGCACAAATGGACAAATGGACACAGGACTCAGTGAGACT	1200
Db	1141		
Qy	1201	TTTCAGACCTCGAAAGTTTCATAA	1224
Db	1201		
Qy	1224	TTTCAGACCTCGAAAGTTTCATAA	1224

RESULT 2				
AX303183				
LOCUS	AX303183	1224 bp	DNA	linear
DEFINITION	Sequence 8 from Patent WO0181557.			
ACCESSION	AX303183			
VERSION	AX303183.1	GI:17383667		
				PAT 30-NOV-2001

KEYWORDS	Homo sapiens (human)
SOURCE	Homo sapiens
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 Hu, Y., Nepomnichy, B., Wang, X., Donoho, G., Scoville, J. and Walke, D.W.
AUTHORS	Human kinase proteins and polynucleotides encoding the same
TITLE	Patent: WO 0181557-A 8 01-NOV-2001;
JOURNAL	Lexicon Genetics Incorporated (US)
FEATURES	Location/Qualifiers
source	1..1224
ORIGIN	/organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"
Query Match	100.0%; Score 1224; DB 6; Length 1224;
Best Local Similarity	100.0%; Pred. No. 8.2e-311;
Matches 1224; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 ATGGAGGCCACACTTCAAGAAACACCAACAGTGTTCATGAAATGAAGATGCAACTTT 60
Db	1 ATGGAGGCCAACACTTCAAGAAACACCAACAGTGTTCATGAAATGAAGATGCAACTTT 60
Qy	61 GACCACCTTTGAAATTTTCGAGCCATTTGGGAAAGGCCAGTTTTCGGAAAGGTCTGCAATGTA 120
Db	61 GACCACCTTTGAAATTTTCGAGCCATTTGGGAAAGGCCAGTTTTCGGAAAGGTCTGCAATGTA 120
Qy	121 CAGAAGAATGATACCAAGAAAGATGACGCAATGAAGTACATGATAAACAAGTGGCGTG 180
Db	121 CAGAAGAATGATACCAAGAAAGATGACGCAATGAAGTACATGATAAACAAGTGGCGTG 180
Qy	181 GAGCGCAATGAGTGAAGATGCTTCAAGGAACTCCAGATCATGCAAGGCTCTGGAGCAC 240
Db	181 GAGCGCAATGAAGTGAAGATGCTTCAAGGAACTCCAGATCATGCAAGGCTCTGGAGCAC 240
Qy	241 CCTTTCCTGTTAAATTTGTGTATTCCTTCCAAGATGAGGAAGACATGTTTCATGGTGGTG 300
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DEFINITION Sequence 12 from patent US 6617147.
ACCESSION AR393904
VERSION AR393904.1 GI:40121081
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  1 (bases 1 to 1675)
AUTHORS Hu,Y., Nepomnichy,B., Wang,X. and Donoho,G.
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QY 181 GAGGCGAATGAAGTGAGAAATGTCTTCAAGGAACTCCAGATCATGCGGGTCTGGAGCAC 240
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LOCUS AX303187 1675 bp DNA linear PAT 30-NOV-2001
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AX303185

LOCUS

DEFINITION Sequence 10 from Patent WO0181557.

1191 bp

DNA

linear

PAT 30-NOV-2001

AX303185

AX303185.1 GI:17383668

VERSION

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FEATURES

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Query Match

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KEYWORDS      Homo sapiens (human)
SOURCE        Homo sapiens
ORGANISM      Homo sapiens
REFERENCE     1
AUTHORS       Gururajan, R., Hafalia, A.J., Patterson, C., Tribouley, C.M.,
              Azimzai, Y., Ding, L., Yao, M.G., Yue, H., Au-Young, J., Bandman, O.,
              Baughn, M.R., Burford, N., Burrill, J.D., Elliott, V.S., Gandhi, A.R.,
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              Zingler, K.A., Marcus, G.A., Nguyen, D.B., Policky, J.L., Ramkumar, J.,
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              Human kinases
TITLE         Patent: WO 0218557-A 44 07-MAR-2002;
JOURNAL       Incyte Genomics Inc. (US)
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QY 781 CTGGAACCTAATCAGACCAACAGATTTTCTCAGTTATCTGATGTCAGAACTTCCCGGTAT 840
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QY 841 ATGAATGATATAAATCTGGGATGAGTGTTCATGAGAAGGCTCATTTCCAGGTTTCATTCCT 900
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QY 1141 GAACAAACCAAGACCCACCAAGTGACAAATGGACAAATGGACA 1183
DB 1544 GAACAAACCAAGACCCACCAAGTGAGGATGGTCAGAAATACA 1586
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LOCUS      AX320936 1191 bp DNA linear PAT 14-DEC-2001
DEFINITION Sequence 3 from Patent WO0181589.
ACCESSION  AX320936
VERSION     AX320936.1 GI:17902482
KEYWORDS    Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE    1
AUTHORS      Meyers, R. and Hunter, J.J.
TITLE        14911 novel protein kinase molecules and uses therefor
JOURNAL      Patent: WO 0181589-A 3 01-NOV-2001;
              Millennium Pharmaceuticals, Inc. (US)
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Best Local Similarity 99.0%; Pred. No. 5.7e-295;
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ACCESSION AR432044
VERSION AR432044.1 GI:40194241
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1485)
AUTHORS Ye,J., Yan,C., Di Francesco,V. and Beasley,E.M.
TITLE Isolated human kinase proteins
JOURNAL Patent: US 6653117-A 1 25-NOV-2003;
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Best Local Similarity 98.8%; Pred. No. 46-294;
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QY 121 CAGAAGATGATACCAAGAGATGTACGCAATGAATGATGAAATGAAGATGTCAAGTGTG 180
Db 123 CAGAAGATGATACCAAGAGATGTACGCAATGAATGATGAAATGAAGATGTCAAGTGTG 182

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QY 661 AGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAAATTTGTACACACGTTTGAGACG 720
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QY 1141 GAACAAACCAAGACCCCAAGTGAGGATGGTCAAGATAACA 1185
Db 1143 GAACAAACCAAGACCCCAAGTGAGGATGGTCAAGATAACA 1185

RESULT 13
AX833107 2063 bp DNA linear PAT 15-DEC-2003
LOCUS AX833107
DEFINITION Sequence 231 from Patent EP1347046.
ACCESSION AX833107
VERSION AX833107.1 GI:39919242
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Isogai,T., Sugiyama,T., Otsuki,T., Wakamatsu,A., Sato,H., Ishii,S., Yamamoto,J.I., Isono,Y., Hio,Y., Otsuka,K., Nagai,K., Irie,R., Tamechika,I., Seki,N., Yoshikawa,T., Otsuka,M., Nagahari,K. and Masuko,Y.
TITLE Full-length cDNA sequences
JOURNAL Patent: EP 1347046-A 231 24-SEP-2003;
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Best Local Similarity 99.7%; Pred. No. 2.6e-260;
Matches 1034; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGGGAGCCAAACATTCAGAAACACACAGTGTGTGATGAAATGAAGATGTCAACTTT 60
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QY 61 GACCACTTTGAAATTTTGGAGCCATTGGGAAAGGACGTTTTGGGAAAGTCTGCAATGTA 120
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Db 541 GCTGGCACCAGCCTTACATGGCACCTGAGATGTTACAGCTCCAGAAAAGGAGCAGGCTAT 600
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Job time : 3718 secs

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OM nucleic - nucleic search, using sw model

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Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	948.6	77.5	2477	3 AK044474	AK044474 Mus muscu
3	948.6	77.5	3766	3 AK036266	AK036266 Mus muscu
4	710.6	58.1	893	4 BG036777	BG036777 602286992
5	556.8	45.5	3439	3 AK082468	AK082468 Mus muscu
6	555.2	45.4	1245	9 AY406286	AY406286 Mus muscu
7	542.4	44.3	1245	9 AY406284	AY406284 Homo sapi
8	535.4	43.7	1245	9 AY406285	AY406285 Pan trogl
9	497.6	40.7	2161	3 AK046439	AK046439 Mus muscu
10	484.8	39.6	1907	3 CR595271	CR595271 full-leng
11	465.6	38.0	829	5 BU156055	BU156055 AGENCOURT
12	457.4	37.4	836	5 BU412592	BU412592 603155332
13	426.4	34.8	869	4 BG033516	BG033516 602302120
14	423.2	34.6	1072	4 BM908009	BM908009 AGENCOURT
15	408.8	33.4	724	6 CR522564	CR522564 UI-M-GHO-
16	392	32.0	711	6 CA320851	CA320851 UI-M-FW0-
17	378	30.9	1003	5 BU146507	BU146507 AGENCOURT
18	375.8	30.7	922	5 BX401698	BX401698 BX401698
19	375.2	30.7	648	6 BY726568	BY726568 BY726568
20	368.4	30.1	664	2 BF472636	BF472636 UI-M-BH3-
21	367.2	30.0	990	5 BX384945	BX384945 BX384945
22	363.8	29.7	1063	5 BQ925566	BQ925566 AGENCOURT
23	359.6	29.4	1104	5 BX416707	BX416707 BX416707
24	355.8	29.1	773	4 BI917132	BI917132 603181546

25	354	28.9	653	7 CF978109	CF978109 F24D11.08
26	349.8	28.6	868	7 CF736437	CF736437 UI-M-HD0-
27	348.2	28.4	643	2 BB629092	BB629092 BB629092
28	344	28.1	667	2 BB642433	BB642433 BB642433
29	342.8	28.0	862	2 BE567816	BE567816 601340485
30	340.4	27.8	882	5 BX342288	BX342288 BX342288
31	337.6	27.6	778	7 CK314110	CK314110 SB0203281
32	336.4	27.5	1000	4 BG824303	BG824303 602727322
33	331.6	26.3	989	5 BX384918	BX384918 BX384918
34	316.4	25.8	769	5 BQ571307	BQ571307 UI-M-FCO-
35	315.6	25.8	609	7 CR452941	CR452941 CR452941
36	308.8	25.2	449	5 BQ044851	BQ044851 UI-M-EHOP
37	296	24.2	851	6 CA454976	CA454976 AGENCOURT
38	292.4	23.9	869	4 BG719068	BG719068 602699189
39	290.8	23.8	725	6 CD578874	CD578874 UI-M-GMO-
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41	283.4	23.2	672	5 BX917647	BX917647 BX917647
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ALIGNMENTS

RESULT 1	AK042599	1927 bp	mrna	linear	HTC 03-APR-2004
LOCUS	AK042599	Mus musculus	7 days neonate cerebellum cDNA	RIKEN full-length	
DEFINITION	AK042599	enriched library, clone:A73009C22 product:SIMILAR TO SERINE	THREONINE KINASE 32 homolog [Homo sapiens], full insert sequence.		
ACCESSION	AK042599	GI:26335202			
VERSION	AK042599	HTC; CAP trapper.			
KEYWORDS	HTC; CAP trapper.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	1	Carninci, P. and Hayashizaki, Y.			
AUTHORS	1	Carninci, P. and Hayashizaki, Y.			
TITLE	1	High-efficiency full-length cDNA cloning			
JOURNAL	1	Meth. Enzymol. 303, 19-44 (1999)			
MEDLINE	99279253				
PUBMED	10349636				
REFERENCE	2	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.			
AUTHORS	2	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.			
TITLE	2	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes			
JOURNAL	2	Genome Res. 10 (10), 1617-1630 (2000)			
MEDLINE	20499374				
PUBMED	11042159				
REFERENCE	3	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.			
AUTHORS	3	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.			
TITLE	3	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer			
JOURNAL	3	Genome Res. 10 (11), 1757-1771 (2000)			
MEDLINE	20530913				
PUBMED	11076861				
REFERENCE	4	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.			
AUTHORS	4	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.			
TITLE	4	Functional annotation of a full-length mouse cDNA collection			
JOURNAL	4	Nature 409, 685-690 (2001)			
PUBMED	11076861				
REFERENCE	5	The FANTOM Consortium and the RIKEN Genome Exploration Research			

TITLE	Group Phase I & II Team.	
	Analysis of the mouse transcriptome based on functional annotation	
JOURNAL	of 60,770 full-length cDNAs	
	Nature 420, 563-573 (2002)	
REFERENCE	6 (bases 1 to 1927)	
	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishii, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saichou, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.	
TITLE	Direct Submission	
	Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)	
COMMENT	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.	
	Please visit our web site for further details. URL: http://genome.gsc.riken.jp/ URL: http://fantom.gsc.riken.jp/ Location/Qualifiers 1. 1927 /organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6J" /db_xref="PANTOM DB:A730009C22" /db_xref="taxon:10090" /clone="A730009C22" /tissue_type="cerebellum" /clone_lib="RIKEN full-length enriched mouse cDNA library" /dev_stages="7 days neonate" 356. .1552 /note="unnamed protein product; SIMILAR TO SERINE THREONINE KINASE 32 homolog [Homo sapiens] (SPTR AAH21666, evidence: PASTY, 95.5%ID, 94.5%length, match=471). putative" /codon_start=1 /protein_id="BAC31302.1" /db_xref="GI:26335203" /translation="WGANTSAPVDFEDNVDNFDHPEILRAIGKSGFGKVICVRKND TKYMYAMKMKQKVERNEVNFKEIQMGLEHPELVNLYSFQDEDFMFWDL LIGDLRHLQONHFQEDTVKLFICELAMALDYLOSRIHHRDMKPNILLDHGHV HITDFNIAAMLPKTRITTVAGTTPYAPENFTSRKETGYSFVDFWNSLGVATVELLR GRPPYHSRSTSSKEIVNMFETAI VTPSAQSWVSLKKLLEPNDFRSHLTDIQ NPPYMSDMNDVAVLQKRLIPGFIPTKGRINDPFTFEEMLEKSLPHKKKRLAKRE KEMKSDSSQCLLIQELHDAVQKEFLIFNREKVSDFNQRQANLALEQTKNTEED QQNNL"	
CDs	356. .1552	
	/note="unnamed protein product; SIMILAR TO SERINE THREONINE KINASE 32 homolog [Homo sapiens] (SPTR AAH21666, evidence: PASTY, 95.5%ID, 94.5%length, match=471). putative"	
ORIGIN	Query Match 77.5%; Score 948.6; DB 3; Length 1927; Best Local Similarity 88.8%; Pred. No. 4.2e-252; Matches 1026; Conservative 0; Mismatches 129; Indels 0; Gaps 0;	
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	181 GAGCGCAATGAAGTGAAGAAATGCTTCAAGGAATCTCAGATCATGCAAGGCTCTGGACAC 240 536 GAGCGGAATGAAGTGAAGAAATGCTTCAAGGAATCTCAGATCATGCAAGGCTCTGGACAC 595 	
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	301 GACCTCTCTGTTGGTGGAGACCTCGGTATCACCTGCAACAGAACGTCCTCAAGGAA 360 656 GACCTGCTACTCGGTGGTGGACCTCGGTATCACCTGCAACAGAACGTCCTCAAGGAA 715 	
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Qy	601 TCCTTTGCTGTGACTGCTGGTCCCTGGGAGTACGGCATATGAACCTGCTGAGAGGCGG 660 956 TCCTTTGCTGTGACTGCTGGTCCCTGGGAGTACGGCATATGAACCTGCTGAGAGGCGG 1015 	
	661 AGACCGTATCATATTCCTCGTACGATCTCCAGCAAGAAATTTGACACACGTTTGAGACG 720 1016 AGACCATATCATACTCCGCTCCAGTACTTCCAGCAAGAAATTTGTAACATGTTTGAGACA 1075 	
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RESULT 2
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DEFINITION
Mus musculus adult retina cDNA, RIKEN full-length enriched library,
clone: A930015B13 product: SIMILAR TO SERINE THREONINE KINASE 32
homolog (Homo sapiens), full insert sequence.
ACCESSION
AK044474.1 GI:26336516
KEYWORDS
HTC; CAP trapper.
SOURCE
Mus musculus
ORGANISM
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
MEDLINE
10349636
PUBMED
2
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374
MEDLINE
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PUBMED
3
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunaga, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
MEDLINE
11076861
PUBMED
4
The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
5
The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 2477)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hasegawa, T., Hara, A., Hashizume, W.,
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Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
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Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp,
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)

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COMMENT
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Retina RNA was provided by Dr. Stefano Gustincich (Department of
Neurobiology, Harvard Medical School, 220 Longwood Ave., Boston, MA
02115, USA) whose assistance is gratefully acknowledged. Please
visit our web site for further details.
URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/.
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evidence: FASTY, 95.5%ID, 94.5%length, match=471)
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Best Local Similarity 88.8%; Pred. No. 4.5e-252;
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Db 252 ATGGAGGCCAACACTTCAAGCAAGCCAGTGTGTTGATGAAATGAAGATGTCACACTTT 311
Qy 61 GACCACCTTGAATTTTGGAGCCATTTGGGAAAGGAGTGTGTTGGAGAGTCTGCATTGTA 120
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Qy 181 GAGCGCAATGAAGTGAAGAAATGTCTTCAAGAACTCCAGATCATCGAGGCTTGAGGAC 240
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Qy 241 CCTTCTCGTGTATTTGTGTGTTATCTCTCAAGATGAGGAGATGTTTCATGTTGTTG 300
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Qy 721 ACTGTTGTAACCTTACCCTTCTGCTGCTGTCACAGGAAATGGTGTCACCTTCTTAAAGCTA 780
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RESULT 3
AK036266
LOCUS
DEFINITION
Mus musculus 16 days neonate cerebellum cDNA, RIKEN full-length
enriched library, clone:9630050F05 product:SIMILAR TO SERINE
THREONINE KINASE 32 homolog [Homo sapiens], full insert sequence.
ACCESSION
AK036266
VERSION
AK036266.1 GI:26331271
KEYWORDS
HTC; CAP trapper.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1
REFERENCE
Carninci, P. and Hayashizaki, Y.
TITLE
High-efficiency full-length cDNA cloning
JOURNAL
Meth. Enzymol. 303, 19-44 (1999)
MEDLINE
99279253
PUBMED
10349636
REFERENCE
2
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
THREONINE KINASE 32 homolog [Homo sapiens] (SPTT/AAH21666,
```

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Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374
11042159
3
Shibata, K., Itoh, M., Aizawa, K., Nagasaka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsuami, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
11076861
4
The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
5
The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 3766)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
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Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan [E-mail:genome-res@gsc.riken.jp,
URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216]
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
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Best Local Similarity 88.8%; Pred. No. 5.1e-252;
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RESULT 4
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 893)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM10041 row: h column: 24
High quality sequence stop: 764.

FEATURES
source

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insert size 2.5 kb and normalized to ROT 5. This is a  
primary library enriched for full-length clones and  
constructed using the Cap-trapper method (Carninci, in  
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(NIH/NHGRI, National Institutes of Health). Note: this
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Db GACCTGCTGTTGGTGGGAGCTGGGTATACCTGCAACAGAAAGTGTGCACTTCCACAGAG 728
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LOCUS Mus musculus HCM2506 gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION AY406286
VERSION AY406286.1 GI:39762260
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 1245)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarimal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferrera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1245)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarimal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferrera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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Best Local Similarity 69.9%; Pred. No. 9.6e-143;
Matches 781; Conservative 0; Mismatches 328; Indels 9; Gaps 2;

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DB 1 ATGGCGGGGAACCACTCCCAACAGCCCGCTGTTGATGAAGAAAGTCAACTTT 60

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QY 775 AAGTACTTCGAACTTAATTCAGACCAACAGATTTTCTCAGTTATCTGATGTCAGAACTTC 834
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RESULT 7
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LOCUS Homo sapiens HCM2506 gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION AY406284
VERSION AY406284.1 GI:39762258
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1245)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1245)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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Best Local Similarity 69.1%; Pred. No. 3.5e-139;
Matches 773; Conservative 0; Mismatches 336; Indels 9; Gaps 2;

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DB 1 ATGGCGGGGAACCACTCCCAACAGCCCGCTGTTGACGAGAATGAGGAAGTCAACTTT 60

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Db 1081 GAATTCATATTTCAACAGAGAGAGCTCAGAGGCA 1118
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RESULT 8

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LOCUS AY406285 1245 bp DNA linear GSS 12-DEC-2003
DEFINITION Pan troglodytes HCM2506 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION AY406285
VERSION AY406285.1 GI:39762259
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
1 (bases 1 to 1245)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
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Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
Science 302 (5652), 1960-1963 (2003)
14671302
2 (bases 1 to 1245)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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gene
ORIGIN
Query Match 43.7%; Score 535.4; DB 9; Length 1245;
Best Local Similarity 68.2%; Pred. No. 3.1e-137; Mismatches 346; Indels 9; Gaps 2;
Matches 763; Conservative 0;
Qy 1 ATGGGAGCCAACTTCAAGAAAACCAACCAAGTGTGTTGATGAAAATGAAGATGTCAACTTT 60
Db 1 ATGGGCGGGAACCACTCCACAGCCCCCGTGTTCAGAGNATGAGNAGTCAACTTT 60
Qy 61 GACCATTGAAATTTTTCGAGCCATTGGGAAAGCGAGTTTGGGAAGGTCTGCATTTGA 120
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full-length enriched library, clone:B230385A21 product:hypothetical
serine/threonine protein kinase, full insert sequence.
ACCESSION
AK046439
VERSION
AK046439.1 GI:26338088
KEYWORDS
HTC; CAP trapper.
SOURCE
Mus musculus
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
10349636
2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374
11042159
3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsumai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yanamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsumura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
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TITLE
JOURNAL
MEDLINE
PUBMED
AUTHORS
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsumai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yanamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsumura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
11076861
4
TITLE
JOURNAL
MEDLINE
PUBMED
AUTHORS
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsumai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yanamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsumura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
11076861
4

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AUTHORS

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JOURNAL

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AUTHORS

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JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)

The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

6 (bases 1 to 2161)

Adachi, J., Furuno, M., Kanamura, T., Hara, A., Hashizume, W., Fukuda, S., Aizawa, K., Hiramoto, K., Hiraoka, T., Hirozane, T., Hayashida, K., Hayatsu, N., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akai, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

Direct Submission

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL: http://genome.gsc.riken.jp/

URL: http://fantom.gsc.riken.jp/

Location/Qualifiers

1. 2161

/organism="Mus musculus"

/mol_type="mRNA"

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/clone="B230385A21"

/sex="male"

/tissue_type="corpora quadrigemina"

/clone_lib="RIKEN full-length enriched mouse cDNA library"

/dev_stage="adult"

110. 1576

/note="unnamed protein product; hypothetical serine/threonine protein kinase (LocustLink[57740, GB|NM_021302, evidence: BLASTN, 99%, match=2159) putative"

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Query Match 40.7%; Score 497.6; DB 3; Length 2161;

Best Local Similarity 67.4%; Pred. No. 1.2e-126;

Matches 736; Conservative 0; Mismatches 344; Indels 12; Gaps 2;

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Db 350 CCGTGTGTTGACAGAGGAGCGTGAATTTTGACCACTTCAGATTTCTGAGAGCAATT 409
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Qy 148 GCAATGAAGTACATGAATAAACAAGTGTGAGGCGCAATGAAGTGAAGAAATGTCTTC 207
Db 470 GCCATGAAGTACATGAATAAACAAGTGTGAGGCGGGATGAGGTCGGGAATGTCTTC 529
Qy 208 AAGAACTCCAGATCATGCGAGGCTGAGAGACCTTTCTGGTAAATTTTGTGTATTC 267
Db 530 CGGAGCTGGAGATCTTACAGAAATCAGCATGTCTTCCTGGTGAACCTCTGTATCTCC 589
Qy 268 TTCCAAGATGAGGAAGACATGTTTCATGTTGTGGACCTCTCTGGTGGAGACTGCGT 327
Db 590 TTCCAGGATGAGGAGACATGTTTCATGTTGTGGATCTGCTTCTGGGGGAGACTGGC 649
Qy 328 TATCACTGCAACAGAGCTCCATTTCAAGAGAAACAGTGAAGCTTTCATCTGTGAG 387
Db 650 TACCACCTACAGCAGAAATGTCAGTTCTCAGAGGACACAGTGAGGCTGTACATCTGTGAG 709
Qy 388 CTGTCATGCGCCCTGGACTACTCTGAGAACAGCGCATCTTTCAGGGATATGAAGCT 447
Db 710 ATGCGCCCTGGCCCTGGACTACTCTGGTAGGCAACACATCATCCACAGAGATGTCAAGCCT 769
Qy 448 GACAATATTTTACTTGACGAACATGGGACGTCGACATCACAGATTTCAACATTTCTGGCG 507
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Qy 568 GAGATGTTACGTC-----CAGAAAGGACGAGCTATTCTTCTGTTGATCTGGTGG 621
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Db 950 TCGTGGGGGTGATGGCTTTACGAGTCTGACAGATGGAGACCTCAGATATCAACTCG 1009
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Db 1070 ACCTGGTCCAAGGAGATGGTAGCCCTGTGCGAAAGCTCCTCACCGTGAACCTTGAGCAC 1129
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Qy 862 GCAGTTTTTCAAGAGGCTCATTCAGGTTTCAATCTCTAATAAGGCGAGCTGAATGT 921
Db 1190 GACCTGAGTGAAGAGGTGGAGCGGCTTTGTGCCAATTAAGGCGGCTGCACTGT 1249
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Db 1250 GATCCCACTTTGAGCTGGAGAGATGATCTTGAGTCGAGGCTCTGCAACAAGAGAA 1309
Qy 982 AAGCGTCTGGCAAGAGGAGAGATATAGGAAATGCGATTTCTTCACAGATGCTT 1041
Db 1310 AAGCGCTGGCAAGAAATTAAGTCTCGGACAGCAGCAGACAGTTCCTCAGTCGGAGAT 1369
Qy 1042 -----CTTCAAGAGCCTTGACTCTGTCAGAGGAGGTTTCAATTTTCAACAGAGAA 1095
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Qy 1096 AAGCTAAACAGG 1107
Db 1430 AAGTTGAGAGG 1441

CR595271 1907 bp mRNA linear HTC 21-JUL-2004
full-length cDNA clone CS0DL006YN16 of B cells (Ramos cell line)
LOCUS Cot 25-normalized of Homo sapiens (human).
DEFINITION CR595271
VERSION CR595271.1 GI:50476078
KEYWORDS HTC; CNSLT cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1907)
AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
REFERENCE 2 (bases 1 to 1907)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
COMMENT - Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life technologies, a
division of Invitrogen.
FEATURES
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/clones="CS0DL006YN16"
/tissue_type="B cells (Ramos cell line) Cot 25-normalized"
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Best Local Similarity 66.7%; Pred. No. 4.2e-123;
Matches 728; Conservative 0; Mismatches 352; Indels 12; Gaps 2;

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Db 228 GGGAAAGCAGCTTTTGGCAAGGTGTGCATTTGTGAGAGCGGGACACAGAGAGATGTAC 287
Qy 148 GCAATGAAGTACATGAATAAACAAGTGTGAGGCGCAATGAAGTGAAGAAATGTCTTC 207
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Db 348 CGGAGCTGGAGATCTCTCGAGGAGATCGACACGCTCTTCCTGGTGAACCTCTGTACTCC 407
Qy 268 TTCCAAGATGAGGAGACATGTTTCATGTTGTGAGACCTCTCTGGTGGAGACTGCGT 327
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Qy 328 TATCACTGCAACAGAGACGTCCTCACTTCAAGAGAAACAGTGAAGCTTCTCATCTGTGAG 387
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QY 388 CTGTCATGCGCCCTGAGTACTCTGCAGAAACGAGCGCATCATTCACAGGATATGAAGCCT 447
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 QY 568 GAGATGTTTCACTC-----CAGAAAGGAGCAGGCTATTCTTTGCTGTTGACTGGTG 621
 Db |||||
 QY 708 GAGATCTTCCACTCTTTTGTCAACGGCGGGACCGGTACTCTCTCGAGGTGAGCTGGTG 767
 Db |||||
 QY 622 TCCCTGGAGTGACGGCATATGAATCTGCTGAGGCCGAGACCGTATCATATTGCTGCC 681
 Db |||||
 QY 768 TCGTGGGGGTGATGGCTATGAGTCTGCTGAGGATGAGGCGCCCTATGACATCCACTCC 827
 Db |||||
 QY 682 AGTACTCTCCAGCAAGGAAATGTACACAGCTTTGAGACGACTGTTGTAACTTACCCTTCT 741
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 5', mRNA sequence.
 ACCESSION BU156055
 VERSION BU156055.1 GI:22669587
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 829)
 AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: ATCC/DCTD/DTF
 cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LHAM3519 row: o column: 22
 High quality sequence start: 7
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 Average insert size 2 kb. Library constructed by Life
 Technologies."

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Query Match 38.0%; Score 465.6; DB 5; Length 829;
 Best Local Similarity 99.2%; Pred. No. 7.1e-118;
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 QY 253 ATGGAGCGAACACTTCAAGAAACACCACTGTTTCATGAAATGAAGATGTCAACTTT 312
 Db |||||
 QY 61 GACCACCTTCAAAATTTTCGAGCCATTTGGGAAAGCGAGTTTGGGAAAGTCTGCAATGTA 120
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 QY 313 GACCACCTTGAATTTTCGAGCCATTTGGGAAAGCGAGTTTGGGAAAGTCTGCAATGTA 372
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 QY 181 GAGCGCAATGAAGTGAAGATGTTTCAAGGAACTCCAGATCATGCAAGGTTCTGAGCAC 240
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 QY 241 CCTTCTCTGTTAATTTGTGTTATCTTCAAGATGAGGAAAGATGTTTCATGTTGGTG 300
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 QY 301 GACCTCTCTGTTGAGACCTGCGTTATCCTGCAACAGACGTCCTTCAAGGAA 360
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 QY 361 GAAACAGTGAAGCTCTTTCATCTGTGAGCTGTGATGCCCTGAGTACCTGCAACCCAG 420
 Db |||||
 QY 613 GAAACAGTGAAGCTCTTTCATCTGTGAGCTGTGATGCCCTGAGTACCTGCAACCCAG 672
 Db |||||
 QY 421 CGCATCATTCACAGGATATGAAGCTTCAACATATTTTACTTGCAGCAATG 472
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 QY 673 CGCATCATTCACAGGATATGAAGCTTCAACATATTTTACTTGCAGCAATG 724
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RESULT 12
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 ACCESSION BU412592
 VERSION BU412592.1 GI:25905263
 KEYWORDS EST.
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.

REFERENCE
1 (bases 1 to 836)
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
22335334
MEDLINE
PUBMED
12445392
COMMENT
Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.

FEATURES
source
1..836
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/strain="layer"
/db_xref="taxon:9031"
/clone="CHEST168p8"
/sex="Female"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="CSEQRBL05"
/note="Organ: ovary; Vector: pBluescript II KS(+); Site: 1:
EcoRI; Site 2: NotI; Modification of pBluescript II KS(+)
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cloned cDNA libraries from messenger RNA for improved 3'
end DNA sequencing by Glenn Fu, et al. U.S. Patent #
6,387,624). Cut pBluescript II KS(+) with NotI and EcoRI.
Ligate in double stranded adaptor containing BspI and
BamHI sites [5'gcccgcgtgcagccgcgacccgataaagaaag
[5'aattcttttttcggtccgggtgcgcgc]

RESULT 13
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DEFINITION
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mRNA sequence.
ACCESSION
BG033516
VERSION
BG033516.1 GI:12425892
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
REFERENCE
1 (bases 1 to 869)
NIH-MGC <http://mgi.nci.nih.gov/>,
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: rgs@bhs-rcmail.nih.gov
Tissue Procurement: DCTD/DTF
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM10114 row: g column: 05
High quality sequence stop: 593.
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Site 2: SalI; Cloned unidirectionally; oligo-dm primed.
Average insert size 1.383 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

FEATURES
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/notes="Organ: breast; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dm primed.
Average insert size 1.383 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

ORIGIN
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Best Local Similarity 98.9%; Pred. No. 5.7e-107;
Matches 471; Conservative 0; Mismatches 1; Indels 4; Gaps 4;
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61 GACCACCTTGAATTTTCCGAGCCATTGGGAAAGGCGAGTTTGGGAAGGCTGCAATTGTA 120
265 GACCACCTTGAATTTTCCGAGCCATTGGGAAAGGCGAG-TTTGGGAAGGCTGCAATTGTA 323

Qy 481 CACATCACAGATTTCACATTTGCGATGCTGCCAGGAGACACAGATTACCACCATG 540
Db 557 CACATCAGTACTTCAACATCGCCAAATGCTGCTAAAGAAACACAGTCAGCCCAAT 616
Qy 541 GCTGGCACCACCAAGCCTTACATGGCACCTGAGATGTTTCAGCTCCAGAAAGGAGCGGTAT 600
Db 617 GCTGGCAGCAAGCCGTACATGGCACCTGAGATGTTTCAGCTCCAGAAACCAATCGGTAT 676
Qy 601 TCCTTTGCTGTTGACTGGTGGTCCCTGGGAGTACGCGCATATGAATGCTGAGAGGCGG 660
Db 677 TCCTTTGCTGAGGACTGGTGGACGCTGGGAATCACTGCTATGAGCTGCTCAGAACCCGG 736
Qy 661 AGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAA 699
Db 737 AGCCGGAACCATATTCAATCAATCATTCACAAATGAA 775

RESULT 13
BG033516
LOCUS
DEFINITION
602302120P1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:4403740 5',
mRNA sequence.
ACCESSION
BG033516
VERSION
BG033516.1 GI:12425892
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
REFERENCE
1 (bases 1 to 869)
NIH-MGC <http://mgi.nci.nih.gov/>,
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: rgs@bhs-rcmail.nih.gov
Tissue Procurement: DCTD/DTF
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM10114 row: g column: 05
High quality sequence stop: 593.
Location/Qualifiers
1..869
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4403740"
/tissue_type="mammary adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_87"
/notes="Organ: breast; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dm primed.
Average insert size 1.383 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

ORIGIN
Query Match 34.8%; Score 426.4; DB 4; Length 869;
Best Local Similarity 98.9%; Pred. No. 5.7e-107;
Matches 471; Conservative 0; Mismatches 1; Indels 4; Gaps 4;
1 ATGGGAGCCACACTTCAAGAAACACCAAGTGTTCATGAATGAAGTGTCAACTTT 60
205 ATGGGAGCGAACACTTCAAGAAACACCAAGTGTTCATGAATGAAGTGTCAACTTT 264
61 GACCACCTTGAATTTTCCGAGCCATTGGGAAAGGCGAGTTTGGGAAGGCTGCAATTGTA 120
265 GACCACCTTGAATTTTCCGAGCCATTGGGAAAGGCGAG-TTTGGGAAGGCTGCAATTGTA 323

ORGANISM Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 724)
REFERENCE NIH-MGC <http://mgi.nci.nih.gov/>.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL
COMMENT Contact: Robert Straubeberg, Ph.D.
Email: csapbs-remail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/mousefl.html>
this clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
Seq primer: pYX-5.
Location/Qualifiers
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/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:6842871"
/tissue_type="Whole brain"
/dev_stage="1, 5, and 15 days newborn"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH BMAP GH0"
/note="Organ: Brain; Vector: pYX- Asc; Site 1: EcoR I;
Site 2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is CGAAGTGAAT. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."

ORIGIN

Query Match 33.4%; Score 408.8; DB 6; Length 724;
Best Local Similarity 85.5%; Pred. No. 4.3e-102;
Matches 455; Conservative 0; Mismatches 77; Indels 0; Gaps 0;
Qy 624 CCTGGAGTGACGGCATATGAACCTGCTGAGAGCGCGGACCGTATCATATTCGCTCCAG 683
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Qy 684 TACTTCCAGCAGGAATTTGACACAGCTTTGACAGCAGCTGTTCACTTACCCCTTCGC 743
Db 69 TACTTCCAGCAGGAATTTGGAACATGTTTGACACAGCAATTTGTAACCTTACCCCTTCGC 128
Qy 744 CTGCTCAGCAGGAATGGTGTCACCTCTTTAAAAAGCTACTCGAACCTAATCCAGACCAACG 803
Db 129 CTGCTCAGCAGGATGGTATCCCTCTTTAAAAAGCTGCTTGAACCTAATCCAGACCAACG 188
Qy 804 ATTTTCTCAGTTATCTGATGTCCAGAACTTCCCGTATATGAATGATATAAATCGGGATGC 863
Db 189 CTTTCTCAGTTGACTGACATTCAGAAATTTCCCTTACATGAGTGACATGAATCGGGAGCG 248
Qy 864 AGTTTTTCAGAAAGGCTCATTCAGGTTTCATTCCTTAATAAAGCAGCGCTGAATTGTGA 923
Db 249 CGTCTCGAGAAGAGGCTCATTCAGGCTTCATTCGACCAAGGCGAGGCTCAATTGTGA 308
Qy 924 TCCTACCTTTTCAACTTGAAGAAATGATTTTGGAGTCCAAACCTCTACATRAAGAAAAAA 983
Db 309 CCCCACTTTTGAAGTGAAGAAATGATTTTGGAGTCCAAACCTCTTCAAGAAAAAGAA 368

Qy 984 GCGTCTGGCAAGAGGAGGAGGATATGAGGAAATCGGATTTCTTCTCAGACATGTCTTCT 1043
Db 369 ACAGCTGGCTAAAGAGGAGGAGGAAATGAGAAAGTGACTCTCTCAGAGTGCCTTCT 428
Qy 1044 TCAAGAGCACCTTTGACTCTCTGTCAGAAAGGAGTTTCATAATTTTCAACAGAGAAAAAGTAAA 1103
Db 429 TCAAGAGCATCTTGATGCTGTTTCAGAAAGAAATTTATAATTTTCAACAGAGAAAAAGTAAA 488
Qy 1104 CAGGACTTTTAAACAAAAGACAAACCAATCTAGCCTTGGAAACAAACCAAGAC 1155
Db 489 AAGTGACTTTTAATCAGAGACAAGCAAAATCTAGCCTTGGAAACAAACCAAGAAC 540

Search completed: December 20, 2004, 06:41:51
Job time : 2956 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 17, 2004, 09:25:19 ; Search time 70 Seconds

(without alignments)
2085.755 Million cell updates/sec

Title: US-10-620-845-9

Perfect score: 2151

Sequence: 1 MGANTSRKPPVFEDNEVDNF.....VTNGQMDTGLSEFTQTSKVS 407

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq_23Sep04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004as:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2151	100.0	407	5	AAE14260 Novel hum
2	2060	95.8	396	4	AAB85491 Human pro
3	2060	95.8	396	5	AAE14261 Novel hum
4	2060	95.8	396	5	AAE21725 Human PKI
5	2054	95.5	396	5	AAM50334 Human 149
6	2054	95.5	396	8	AD127077 Protein o
7	2047	95.2	396	6	ABg70700 Human ser
8	2047	95.2	396	6	ABu62276 Human kin
9	2047	95.2	396	8	ADL09162 Human pro
10	1880	87.4	398	7	ADf44523 Mouse kin
11	1875	87.2	398	7	ADf44527 Mouse kin
12	1827	84.9	358	7	ADM03989 Human pro
13	1513.5	70.4	327	4	Aau03504 Human pro
14	1430.5	66.5	404	6	ABu62277 Mouse ser
15	1430.5	66.5	404	8	ADL09164 Mouse ser
16	1423.5	66.2	403	6	ABU62278 Human ser
17	1423.5	66.2	403	8	ADL09165 Human ser
18	1423.5	66.2	414	4	AAB65600 Novel pro
19	1423.5	66.2	414	5	ABP43807 Serine/th
20	1423.5	66.2	414	5	AAO17710 Human ser
21	1423.5	66.2	414	6	ABR58617 Human can
22	1423.5	66.2	414	7	ADe38375 Human pro
23	1423.5	66.2	414	8	ADi29205 Human MAR
24	1423.5	66.2	414	8	ADd17598 Human sof
25	1333.5	62.0	419	4	AAB65599 Novel pro

ALIGNMENTS

RESULT 1

AAE14260

ID AAE14260 standard; protein; 407 AA.

XX AAE14260;

DT 07-MAR-2002 (first entry)

DE Novel human protein (NHP) kinase #3.

XX Novel human protein; NHP; gene therapy; diagnosis; drug screening;

KW gene expression; breast cancer; prostate cancer; nutraceutical; cosmetic;

KW medical disorder; mental; biological; physiological; chemotherapeutic.

XX Homo sapiens.

OS WO200181557-A2.

PN 01-NOV-2001.

PD 24-APR-2001; 2001WO-US013149.

XX 25-APR-2000; 2000US-0199499P.

PR 01-MAY-2000; 2000US-0201227P.

XX (LEXI-) LEXICON GENETICS INC.

XX Hu Y, Nepomniichy B, Wang X, Donoho G, Scoville J, Walke DW;

DR WPI; 2002-034442/04.

DR N-ESDB; AAD23678.

XX New nucleic acid molecules encoding new human proteins, useful in diagnosis, drug screening, clinical trial monitoring, treatment of physiological disorders, and cosmetic or nutraceutical applications.

XX Claim 5; Page 41-42; 44pp; English.

XX The invention relates to novel human protein (NHP) kinases and their corresponding cDNA molecules. NHP kinase and its DNA are useful as reagents in assays for screening compounds that can be used as

pharmaceutical and medical disorders, and also as chemotherapeutic agents useful in the treatment of breast cancer and prostate cancer. NHP DNA is useful for diagnosis, drug screening, clinical trial monitoring, the treatment of physiological disorders or diseases, and cosmetic and

nutraceutical applications. NHP DNA is also useful for the identification of coding sequence and the mapping of a unique gene to a particular

26 1333.5 62.0 419 8 ADI29204 Human MAR
27 1333.5 62.0 488 5 AAO17709 Murine se
28 1332.5 61.9 486 8 ADJ96618 Human YAN
29 1332.5 61.9 486 8 ADK71861 Human kin
30 1331 61.9 485 5 AAE24141 Human kin
31 1329.5 61.8 425 4 AAM40592 Mouse pol
32 1328.5 61.8 384 6 ABU62279 Mouse ser
33 1328.5 61.8 384 8 ADL09166 Mouse ser
34 1323.5 61.5 419 4 AAM38806 Human pol
35 1310.5 60.9 488 6 ABO14992 Human NOV
36 1294.5 60.2 399 5 ABB84300 Murine se
37 1294 60.2 713 5 ABB06090 Human NS
38 1272.5 59.2 375 4 AAE04371 Human kin
39 1272.5 59.2 442 7 ADG74653 Human kin
40 1194.5 55.5 444 6 AAE37974 Human kin
41 1191 55.4 364 5 AAO17708 Human ser
42 1186.5 55.2 364 4 AAU29309 Human PRO
43 1186.5 55.2 364 6 ABU58685 Human PRO
44 1186.5 55.2 364 6 ABU88233 Novel hum
45 1186.5 55.2 364 6 ABU84548 Human sec

CC chromosome. NHP DNA is further useful as hybridisation probes for
 CC screening libraries and assessing gene expression patterns, and also for
 CC the detection of mutant NHPs or inappropriately expressed NHPs for
 CC disease diagnosis. NHP DNA is also useful in gene therapy. The present
 CC sequence is novel human protein (NHP) kinase which is similar to
 CC serine/threonine protein kinases, ribosomal protein kinases and cAMP-
 CC dependent kinases related to the invention

XX SQ Sequence 407 AA;

Query Match 100.0%; Score 2151; DB 5; Length 407;
 Best Local Similarity 100.0%; Pred. No. 9.4e-196;
 Matches 407; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGANTSRRPPVFDENEDVNFDFEILRAIGKSGFKVCIVQKNDTKMYAMKYNKQKCV 60
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 QY 61 ERNEVRNVFKELQIMQGLEHPLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKE 120
 DB 61 ERNEVRNVFKELQIMQGLEHPLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKE 120
 QY 121 ETVKLFICELVMDLYLQONRIIHRDKMPDNLIDDEHGHVHTDFNIAAMLPRETQITTM 180
 DB 121 ETVKLFICELVMDLYLQONRIIHRDKMPDNLIDDEHGHVHTDFNIAAMLPRETQITTM 180
 QY 181 AGTKPYMAPEMFSSRKAGYGFVDMWSLGVTVAYELLGRPPYHRSSTSKSVHVFET 240
 DB 181 AGTKPYMAPEMFSSRKAGYGFVDMWSLGVTVAYELLGRPPYHRSSTSKSVHVFET 240
 QY 241 TVVTYPSAWSQEMVSLKLLLEPNPDQRFSDVQNPFPYNDINWDAVFQKRLIPGIP 300
 DB 241 TVVTYPSAWSQEMVSLKLLLEPNPDQRFSDVQNPFPYNDINWDAVFQKRLIPGIP 300
 QY 301 NGRNLNCDPTFELEEMILESPLHKKKRLAKKEDMKRKCDSSTCLLQEHLDVQKEFI 360
 DB 301 NGRNLNCDPTFELEEMILESPLHKKKRLAKKEDMKRKCDSSTCLLQEHLDVQKEFI 360
 QY 361 IFNREKVNDRFNKQPNLALEQTKDPQVTNGQMDTGLSETFTQSKVS 407
 DB 361 IFNREKVNDRFNKQPNLALEQTKDPQVTNGQMDTGLSETFTQSKVS 407

RESULT 2

AAB85491
 ID AAB85491 standard; protein; 396 AA.

XX AC AAB85491;

XX DT 25-SEP-2001 (first entry)

XX DE Human protein kinase SGK177.

XX KW Protein kinase; enzyme; cytostatic; nootropic; neuroprotective; human;
 KW antiparkinsonian; virucide; antibacterial; antifungal; antimigraine;
 KW analgesic; hypotensive; hypertensive; immunosuppressive; antiallergic;
 KW antipsoriatic; antineumatic; antiarthritic; ophthalmological; anorectic;
 KW osteopathic; thrombolytic; antiarteriosclerotic; antiasthmatic;
 KW vasotrophic; antidiabetic; gene therapy.

XX OS Homo sapiens.

XX PN WO200155356-A2.

XX XX 02-AUG-2001.

XX PD 25-JAN-2001; 2001WO-US002337.

XX PR 25-JAN-2000; 2000US-0178078P.

XX PR 31-JAN-2000; 2000US-0179364P.

XX PR 17-FEB-2000; 2000US-0183173P.

XX PR 17-MAR-2000; 2000US-0190162P.

XX PR 29-MAR-2000; 2000US-0193404P.

PR 13-NOV-2000; 2000US-0247013P.

XX PA (SUGE-) SUGEN INC.

XX PI Plowman G, Whyte D, Manning G, Sudarsanam S, Martinez R;

XX DR WPI; 2001-476202/51.

XX DR N-PSDB; AAH46891.

XX KW Kinase polypeptides useful for treating cancers, Alzheimer's disease,
 PT viral infections, diabetes, obesity, organ transplant rejection and
 PT rheumatoid arthritis.

PS Claim 7; Page 214; 218pp; English.

XX The invention provides human protein kinases and protein kinase-like
 CC enzymes and polynucleotides encoding the polypeptides. The kinase
 CC polypeptides and their modulators are useful for treating a disease or
 CC disorder such as cancer, immune-related diseases, cardiovascular disease,
 CC brain or neuronal-associated disease and metabolic disorders, including
 CC cancers of tissues, cancers of hematopoietic origin, diseases of the
 CC central nervous system, diseases of the peripheral nervous system,
 CC Alzheimer's disease, Parkinson's disease, multiple sclerosis, amyotrophic
 CC lateral sclerosis, viral infections, infections caused by prions,
 CC bacteria and fungi, ocular diseases, migraines, pain, sexual dysfunction,
 CC mood disorders, attention disorders, cognition disorders, hypotension,
 CC hypertension, psychotic disorders, neurological disorders, dyskinesias,
 CC metabolic disorders, and organ transplant rejection. They are also useful
 CC for treating rhinitis, autoimmunity, atherosclerosis, psoriasis,
 CC osteoarthritis, asthma, chronic inflammatory pelvic disease, chronic
 CC inflammatory bowel disease, rheumatoid arthritis, metabolic disorders
 CC such as diabetes, obesity, cardiovascular diseases such as reperfusion
 CC injury, coronary thrombosis, clotting disorders and atherosclerosis,
 CC ocular diseases such as glaucoma, retinopathy and macular degeneration,
 CC psychiatric and neurological disorders such as anxiety, schizophrenia,
 CC dementia, manic depression, etc. The polynucleotides are useful in gene
 CC therapy techniques to treat the above mentioned disorders. Sequences
 CC AAB85491-85522 represent the human protein kinases of the invention

XX SQ Sequence 396 AA;

Query Match 95.8%; Score 2060; DB 4; Length 396;

Best Local Similarity 99.2%; Pred. No. 4.2e-187;

Matches 389; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGANTSRRPPVFDENEDVNFDFEILRAIGKSGFKVCIVQKNDTKMYAMKYNKQKCV 60

DB 1 MGANTSRRPPVFDENEDVNFDFEILRAIGKSGFKVCIVQKNDTKMYAMKYNKQKCV 60

QY 61 ERNEVRNVFKELQIMQGLEHPLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKE 120

DB 61 ERNEVRNVFKELQIMQGLEHPLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKE 120

QY 121 ETVKLFICELVMDLYLQONRIIHRDKMPDNLIDDEHGHVHTDFNIAAMLPRETQITTM 180

DB 121 ETVKLFICELVMDLYLQONRIIHRDKMPDNLIDDEHGHVHTDFNIAAMLPRETQITTM 180

QY 181 AGTKPYMAPEMFSSRKAGYGFVDMWSLGVTVAYELLGRPPYHRSSTSKSVHVFET 240

DB 181 AGTKPYMAPEMFSSRKAGYGFVDMWSLGVTVAYELLGRPPYHRSSTSKSVHVFET 240

QY 241 TVVTYPSAWSQEMVSLKLLLEPNPDQRFSDVQNPFPYNDINWDAVFQKRLIPGIP 300

DB 241 TVVTYPSAWSQEMVSLKLLLEPNPDQRFSDVQNPFPYNDINWDAVFQKRLIPGIP 300

QY 301 NGRNLNCDPTFELEEMILESPLHKKKRLAKKEDMKRKCDSSTCLLQEHLDVQKEFI 360

DB 301 NGRNLNCDPTFELEEMILESPLHKKKRLAKKEDMKRKCDSSTCLLQEHLDVQKEFI 360

QY 361 IFNREKVNDRFNKQPNLALEQTKDPQVTNGQ 392

DB 361 IFNREKVNDRFNKQPNLALEQTKDPQVTNGQ 392

```

RESULT 3
AAE14261
ID AAE14261 standard; protein; 396 AA.
XX
AC AAE14261;
XX
DT 07-MAR-2002 (first entry)
XX
DE Novel human protein (NHP) kinase #4.
XX
KW Novel human protein; NHP; gene therapy; diagnosis; drug screening;
KW gene expression; breast cancer; prostate cancer; nutraceutical; cosmetic;
KW medical disorder; mental; biological; physiological; chemotherapeutic.
XX
OS Homo sapiens.
XX
PN WO200181557-A2.
XX
XX 01-NOV-2001.
XX
XX 24-APR-2001; 2001WO-US013149.
XX
XX 25-APR-2000; 2000US-0199499P.
XX
XX 01-MAY-2000; 2000US-0201227P.
XX
PA (LEXI-) LEXICON GENETICS INC.
XX
XX Hu Y, Nepomnichy B, Wang X, Donoho G, Scoville J, Walke DW;
XX
XX WPI; 2002-034442/04.
XX
XX N-PSDB; AAD23679.
XX
XX New nucleic acid molecules encoding new human proteins, useful in
XX diagnosis, drug screening, clinical trial monitoring, treatment of
XX physiological disorders, and cosmetic or nutraceutical applications.
XX
XX Claim 7; Page 43; 44pp; English.
XX
XX The invention relates to novel human protein (NHP) kinases and their
XX corresponding cDNA molecules. NHP kinase and its DNA are useful as
XX reagents in assays for screening compounds that can be used as
XX pharmaceutical reagents useful in the therapeutic treatment of mental,
XX biological and medical disorders, and also as chemotherapeutic agents
XX useful in the treatment of breast cancer and prostate cancer. NHP DNA is
XX useful for diagnosis, drug screening, clinical trial monitoring, and
XX treatment of physiological disorders or diseases, and cosmetic and
XX nutraceutical applications. NHP DNA is also useful for the identification
XX of coding sequence and the mapping of a unique gene to a particular
XX chromosome. NHP DNA is further useful as hybridisation probes for
XX screening libraries and assessing gene expression patterns, and also for
XX the detection of mutant NHPs or inappropriately expressed NHPs for
XX disease diagnosis. NHP DNA is also useful in gene therapy. The present
XX sequence is novel human protein (NHP) kinase which is similar to
XX serine/threonine protein kinases, ribosomal protein kinases and cAMP-
XX dependent kinases related to the invention
XX
XX Sequence 396 AA;
XX
Query Match 95.8%; Score 2060; DB 5; Length 396;
Best Local Similarity 99.2%; Pred. No. 4.2e-187;
Matches 389; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 MGATSRKPPVDFNEDVNFDFHILRAIGKSGFGKVCIVQKNDTKQWAMKYNKQKCV 60
DB 1 MGATSRKPPVDFNEDVNFDFHILRAIGKSGFGKVCIVQKNDTKQWAMKYNKQKCV 60
QY 61 ERNEVRNVFKEIQIMQGLEHPFLVNLWYSFQDEEDFMFVVDLLGDLRLYHLQNVHFK 120
DB 61 ERNEVRNVFKEIQIMQGLEHPFLVNLWYSFQDEEDFMFVVDLLGDLRLYHLQNVHFK 120
QY 121 ETVKLFICELVMALDYLNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETOITTM 180
DB 121 ETVKLFICELVMALDYLNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETOITTM 180
QY 181 AGTKPYMAPEMFSSRKAGYSFAVDWWSLGVTAPELLRGRPPYHIRSTSSKEIVHPTET 240
DB 181 AGTKPYMAPEMFSSRKAGYSFAVDWWSLGVTAPELLRGRPPYHIRSTSSKEIVHPTET 240
QY 241 TVVTYPSAWQEMVSLKLLLEPNPDORFQSLSVQNFPPYMNNDINWDAVFOKRLIPGPIP 300
DB 241 TVVTYPSAWQEMVSLKLLLEPNPDORFQSLSVQNFPPYMNNDINWDAVFOKRLIPGPIP 300
QY 301 NKGRNLCNCDPTFELEEMILESPLHKKKRLAKKEDMRKCDSSQTCLLQEHLDVSQKEFI 360
DB 301 NKGRNLCNCDPTFELEEMILESPLHKKKRLAKKEDMRKCDSSQTCLLQEHLDVSQKEFI 360
QY 361 IFNREKVNDRDNKRPQPNLALEQTKDPQVTNGQ 392
DB 361 IFNREKVNDRDNKRPQPNLALEQTKDPQVEDGQ 392
XX
RESULT 4
AAE21725
ID AAE21725 standard; protein; 396 AA.
XX
AC AAE21725;
XX
DT 16-JUL-2002 (first entry)
XX
DE Human PKIN-20 protein.
XX
KW Human; kinase; enzyme; PKIN-20 protein; immune system disorder; anaemia;
KW acquired immune deficiency syndrome; thymic hypoplasia; Crohn's disease;
KW asthma; neurological disorder; epilepsy; Charcot-Marie-Tooth disease;
KW AIDS; seizures; cell proliferative disorder; cancer; adenocarcinoma;
KW leukaemia; lymphoma; melanoma; myeloma; sarcoma; developmental disorder;
KW Down's syndrome; gene therapy; protein therapy; cytostatic.
XX
OS Homo sapiens.
XX
PH Key Location/Qualifiers
FT Domain 13..300
FT /note= "Protein kinase domain"
FT Domain 23..300
FT /note= "Protein kinase domain"
FT Domain 23..281
FT /note= "Eukaryotic protein kinase domain"
FT Domain 25..270
FT /note= "Protein kinase domain"
FT Domain 25..268
FT /note= "Protein kinase domain"
XX
XX WO200218557-A2.
XX
XX 07-MAR-2002.
XX
XX 31-AUG-2001; 2001WO-US027219.
XX
XX 31-AUG-2000; 2000US-0229873P.
XX
XX 08-SEP-2000; 2000US-0231357P.
XX
XX 14-SEP-2000; 2000US-0232654P.
XX
XX 22-SEP-2000; 2000US-0234902P.
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XX 29-SEP-2000; 2000US-0236499P.
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XX 06-OCT-2000; 2000US-0238389P.
XX
XX 13-OCT-2000; 2000US-0240542P.
XX
XX (INCY-) INCYTE GENOMICS INC.
XX
XX Bandman O, Nguyen DB, Wallia NK, Hafalia AJA, Yao MG, Gandhi AR;
XX Gururajan R, Ding L, Patterson C, Yue H, Baughn MR, Tribouley CM;
XX Thornton M, Elliott VS, Lu Y, Ison CH, Au-Young J, Tang YT;
XX Azimzai Y, Burrill JD, Marcus GA, Zingler KA, Lu DAM, Lal PG;
XX Ramkumar J, Warren BA, Kearney L, Policky JL, Thangavelu K;
XX Burford N;
XX

```

DR WPI; 2002-329769/36.
XX N-PSDB; AAD34317.
XX New human kinases, useful for diagnosing, treating or preventing immune
PT system disorders (e.g. Crohn's disease), neurological disorders (e.g.
PT epilepsy), or cell proliferative disorders (e.g. cancers such as leukemia
PT or lymphoma).
XX
PS Claim 75; Page 184-185; 218pp; English.
XX
CC The present invention relates to human kinases (PKIN) and polynucleotides
CC encoding such proteins. PKIN sequences of the invention are useful for
CC diagnosing, treating or preventing disorders associated with aberrant
CC expression of PKIN, particularly immune system disorders (e.g. acquired
CC immune deficiency syndrome (AIDS), thymic hypoplasia, Crohn's disease,
CC anaemia, asthma), neurological disorders (e.g. epilepsy, Charcot-Marie-
CC Tooth disease or seizures), cell proliferative disorders (e.g. cancers
CC such as adenocarcinoma, leukaemia, lymphoma, melanoma, sarcoma),
CC and developmental disorders (e.g. Down's syndrome). They are also used in
CC gene therapy and protein therapy. The present sequence is human PKIN-20
CC protein
XX
SQ Sequence 396 AA;

Query Match 95.8%; Score 2060; DB 5; Length 396;
Best Local Similarity 99.2%; Pred. No. 4.2e-187;
Matches 389; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGANTSRRPPVDENEDVNFHETLRAIGSGFGKVCIVOKNDTKMYAMKYNKOCV 60
Db 1 MGANTSRRPPVDENEDVNFHETLRAIGSGFGKVCIVOKNDTKMYAMKYNKOCV 60

QY 61 ERNEVRNVFKELQIQMGLHFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQNVHFK 120
Db 61 ERNEVRNVFKELQIQMGLHFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQNVHFK 120

QY 121 ETVKLFICELVMDLYNQRIIHRDKPNDILLDEGHVHITDFNIAAMLPRETQITTM 180
Db 121 ETVKLFICELVMDLYNQRIIHRDKPNDILLDEGHVHITDFNIAAMLPRETQITTM 180

QY 181 AGTPYMAPENFSSRGAGYFVNDWSLGVATVALLGRPPYHIRSTSKETVHTFET 240
Db 181 AGTPYMAPENFSSRGAGYFVNDWSLGVATVALLGRPPYHIRSTSKETVHTFET 240

QY 241 TVVTYPSAWSQEMVSLKLLLEPNPDQRFQSLSDVQNPFPYNDINWDVAFQKRLIPGIP 300
Db 241 TVVTYPSAWSQEMVSLKLLLEPNPDQRFQSLSDVQNPFPYNDINWDVAFQKRLIPGIP 300

QY 301 NKGRINCDDPTFELEMILESPHLKKKRLAKKEDMKRCDSSQTCLLQEHLDVQKEFI 360
Db 301 NKGRINCDDPTFELEMILESPHLKKKRLAKKEDMKRCDSSQTCLLQEHLDVQKEFI 360

QY 361 IFNREKVNDRDNKQPNLALBQTKDPQVNTGQ 392
Db 361 IFNREKVNDRDNKQPNLALBQTKDPQGEDGQ 392

RESULT 5
AAM50334
ID AAM50334 standard; protein; 396 AA.
XX
AC AAM50334;
XX
DT 04-FEB-2002 (first entry)
XX
DE Human 14911 protein kinase.
XX
KW Protein kinase; human; signal transduction; lung cancer; colon cancer;
KW brain cancer; breast cancer; therapy; diagnosis.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers

Modified-site 2..7 /note= "N-myristoylated"
FT
Modified-site 4..7 /note= "Asn is N-glycosylated"
FT
Modified-site 5..7 /note= "O-phosphorylated by protein kinase C"
FT
Domain 23..281 /label= Protein_kinase_domain
FT
Peptide 29..37 /note= "protein kinase ATP-binding region signature"
FT
Modified-site 43..46 /note= "Asn is N-glycosylated"
FT
Modified-site 45..47 /note= "O-phosphorylated by protein kinase C"
FT
Modified-site 89..92 /note= "O-phosphorylated by casein kinase II"
FT
Modified-site 122..124 /note= "O-phosphorylated by protein kinase C"
FT
Active-site 142..154 /note= "active site signal"
FT
Modified-site 193..195 /note= "O-phosphorylated by protein kinase C"
FT
Modified-site 197..202 /note= "N-myristoylated"
FT
Modified-site 212..215 /note= "O-phosphorylated by casein kinase II"
FT
Modified-site 218..221 /note= "Aminated"
FT
Modified-site 230..233 /note= "O-phosphorylated by casein kinase II"
FT
Modified-site 230..232 /note= "O-phosphorylated by protein kinase C"
FT
Domain 282..301 /label= Protein_kinase_C-terminal_domain
FT
Modified-site 391..396 /note= "N-myristoylated"
FT
XX WO200181589-A2.
XX
XX 01-NOV-2001.
PD
XX 25-APR-2001; 2001WO-US013785.
PP
XX 25-APR-2000; 2000US-0199391P.
PR
XX 15-JUN-2000; 2000US-00593927.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Meyers R, Hunter JJ;
XX
XX WPI; 2002-041408/05.
DR
XX N-PSDB; AAI70704.
XX
PT Novel protein kinase nucleic acid molecules and the encoded proteins for
PT diagnosing and treating cellular proliferative, bone, immune,
PT cardiovascular, liver, pain or metabolic disorders and identifying
PT modulators.
XX
XX Claim 4(d); Fig 1A-B; 115pp; English.
PS
XX The present sequence is that of a novel human protein kinase, designated
CC 14911. This protein kinase plays a role in, or functions in, the
CC transduction of signals for cell proliferation, differentiation and
CC apoptosis, modulating the activity of one or more proteins involved in
CC cellular growth or differentiation. 14911 molecules are overexpressed in
CC some tumour cells, where they may inappropriately propagate either cell
CC proliferation or cell survival signals. The invention provides methods
CC for the diagnosis and treatment of cancer, including breast cancer, brain
CC and especially lung cancer (claimed), and methods for evaluating the
CC efficacy of treatment. 14911 polypeptides can be produced by culturing
CC of claimed host cells, and used in claimed methods of identifying 14911
CC modulator compounds. 14911 binding partners are used in claimed methods
CC of identifying subjects at risk of cancer or cellular proliferation

CC and/or differentiation disorders. A claimed method of treating cancer or
CC a cellular proliferation and/or differentiation disorder, especially
CC lung, colon, brain and breast cancer, uses a small molecule, peptide,
CC phosphopeptide, anti-14911 antibody, a 14911 polypeptide or its variant.
CC Other disorders that may be diagnosed/treated include those associated
CC with bone metabolism, autoimmune diseases, cardiovascular disorders,
CC liver disorders, viral diseases, pain and metabolic disorders
XX
SQ Sequence 396 AA;

Query Match 95.5%; Score 2054; DB 5; Length 396;
Best Local Similarity 99.0%; Pred. No. 1.6e-186;
Matches 388; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MGANTSRRKPPVFDENEDVNFDFEILRAIGKSGFGKVCIVQKNDTKMYAMKYNKQKCV 60
Db 1 MGANTSRRKPPVFDENEDVNFDFEILRAIGKSGFGKVCIVQKNDTKMYAMKYNKQKCV 60

Qy 61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEEDFMFVDDLGGDLRYHLQONVHFK 120
Db 61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEEDFMFVDDLGGDLRYHLQONVHFK 120

Qy 121 ETVKLFICELVMDLYLQONQRIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETIQITM 180
Db 121 ETVKLFICELVMDLYLQONQRIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETIQITM 180

Qy 181 AGTKPYNAPEMFSSRKAGYSFAVDWWSLGTAYELLGRPPYHRSSTSKELVHTFET 240
Db 181 AGTKPYNAPEMFSSRKAGYSFAVDWWSLGTAYELLGRPPYHRSSTSKELVHTFET 240

Qy 241 TVVTYPSAWSEMVSLLKLEPNPDORFQSLSQVQNFPPYMNNDINWDAVQKRLIPGIP 300
Db 241 TVVTYPSAWSEMVSLLKLEPNPDORFQSLSQVQNFPPYMNNDINWDAVQKRLIPGIP 300

Qy 301 NKGRLCDPTFELEEMILESKPLHKKKXKLAKEKDMKCDSSOTCLLQEHLDVQKEFI 360
Db 301 NKGRLCDPTFELEEMILESKPLHKKKXKLAKEKDMKCDSSOTCLLQEHLDVQKEFI 360

Qy 361 IFNREKVNDRPNKQPNLALBQTKDPQVNTGQ 392
Db 361 IFNREKVNDRPNKQPNLALBQTKDPQGEDQ 392

RESULT 6
ADL27077
ID ADL27077 standard; protein; 396 AA.
AC ADL27077;
XX
XX 20-MAY-2004 (first entry)
XX
XX Protein of novel human molecule, 14911.
XX
XX 26199; 33530; 33949; 47148; 50226; 58764; 62113; 32144; 32235; 23565;
KW 13305; 14911; 86216; 25206; 8843; cytostatic; haemostatic; gynecological;
KW nephrotropic; dermatological; immunosuppressive; antiinflammatory;
KW hepatotropic; virucide; analgesic; vasotropic; gene therapy;
KW cellular proliferative; differentiative disorder; brain; platelet;
KW breast; colon; kidney; lung; ovarian; prostate; haematopoietic;
KW pancreatic; skeletal muscle; skin; bone metabolism; immune;
KW transgenic animal; chromosome identification; tissue typing; human.
XX
OS Homo sapiens.
XX
XX US2004005664-A1.
XX
XX 08-JAN-2004.
XX
XX 10-APR-2003; 2003US-00410764.
XX
XX 25-APR-2000; 2000US-0199391P.
PR 19-MAY-2000; 2000US-0205301P.
PR 15-JUN-2000; 2000US-00593927.

PR 01-SEP-2000; 2000US-0229300P.
PR 05-OCT-2000; 2000US-0238054P.
PR 11-OCT-2000; 2000US-00866673.
PR 30-NOV-2000; 2000US-0250186P.
PR 16-FEB-2001; 2001US-0269440P.
PR 17-MAY-2001; 2001US-00860352.
PR 06-AUG-2001; 2001US-00924358.
PR 24-AUG-2001; 2001US-0314884P.
PR 27-SEP-2001; 2001US-00966614.
PR 29-OCT-2001; 2001US-0347815P.
PR 29-NOV-2001; 2001US-00997816.
PR 24-JAN-2002; 2002US-0351572P.
PR 15-FEB-2002; 2002US-00076535.
PR 23-AUG-2002; 2002US-00226410.
PR 25-OCT-2002; 2002US-00281094.
PR 24-JAN-2003; 2003US-00350553.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Meyers RE, Macbeth KJ, Curtis RAJ, Rudolph-Owen LA, Weich NS;
PI Olandt P, Tsai F, Kapeller-Libermann R, Carroll JM;
XX
XX WPI; 2004-081724/08.
XX
XX N-PSDB; ADL27076, ADL27078.
XX
XX New isolated 26199, 33530, 33949, 47148, 50226, 58764, 62113, 32144,
PT 32235, 23565, 13305, 14911, 86216, 25206 or 8843 polypeptides and nucleic
PT acids, useful for diagnosing or treating cancer, autoimmune, metabolic
PT and viral diseases.
XX
XX Claim 4; SEQ ID NO 101; 237pp; English.
XX
XX The invention relates to novel nucleic acid molecules designated 26199,
CC 33530, 33949, 47148, 50226, 58764, 62113, 32144, 32235, 23565, 13305,
CC 14911, 86216, 25206 or 8843. The novel nucleic acid molecules and their
CC compositions have the following activities: cytostatic, haemostatic,
CC gynecological, nephrotropic, dermatological, immunosuppressive,
CC antiinflammatory, hepatotropic, virucide, analgesic, and vasotropic. The
CC novel nucleic acid molecules may be used in gene therapy to treat
CC disorders. The methods and compositions of the present invention are
CC useful for the diagnosis, prevention and/or treatment of diseases or
CC conditions associated with aberrant expression or activity of the
CC polypeptides, such as a cellular proliferative and/or differentiative
CC disorder, brain disorder, platelet disorder, breast disorder, colon
CC disorder, kidney (renal) disorder, lung disorder, ovarian disorder,
CC prostate disorder, haematopoietic disorder, pancreatic disorder, skeletal
CC muscle disorder, skin (dermal) disorder, disorder associated with bone
CC metabolism, immune, e.g., inflammatory, disorder, cardiovascular
CC disorder, endothelial cell disorder, liver disorder, viral diseases, pain
CC disorder, metabolic disorder, neurological or CNS disorder, erythroid
CC disorder or anaemic disorder. The compositions may also be used in assays
CC to identify other proteins or molecules involved in binding reaction, to
CC generate transgenic animals or knockout animals, which in turn are useful
CC in the development and screening of therapeutically useful reagents, for
CC chromosome identification, and tissue typing. This sequence represents a
CC protein derived from one of the novel human nucleic acid molecules of the
CC invention.
XX
XX Sequence 396 AA;

Query Match 95.5%; Score 2054; DB 8; Length 396;
Best Local Similarity 99.0%; Pred. No. 1.6e-186;
Matches 388; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MGANTSRRKPPVFDENEDVNFDFEILRAIGKSGFGKVCIVQKNDTKMYAMKYNKQKCV 60
Db 1 MGANTSRRKPPVFDENEDVNFDFEILRAIGKSGFGKVCIVQKNDTKMYAMKYNKQKCV 60

Qy 61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEEDFMFVDDLGGDLRYHLQONVHFK 120
Db 61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEEDFMFVDDLGGDLRYHLQONVHFK 120

Qy 121 ETVKLFICELVMDLYLQONQRIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETIQITM 180

Db 121 ETVKLFICELVWALDYQNRHDMKPDNILLDEGHVHTDFAAAMLPREIQTITM 180
Qy 181 AGTKPYMAPEMSSRRGAGYFAVDWWSLGVYAYELLGRRRPYHRSSTSSKEIVHTTET 240
Db 181 AGTKPYMAPEMSSRRGAGYFAVDWWSLGVYAYELLGRRRPYHRSSTSSKEIVHTTET 240
Qy 241 TVVTYPSAWSQBMVSLKLLLEPNPDQRFPSQLSDVQNFYPMNDINWDAVFOKRLIPGP 300
Db 241 TVVTYPSAWSQBMVSLKLLLEPNPDQRFPSQLSDVQNFYPMNDINWDAVFOKRLIPGP 300
Qy 301 NKGRLNCDFTELEEMILESKPLHKKKRLAKKEDMKRKCDSSTQCLLQEHLDVSQKBEFI 360
Db 301 NKGRLNCDFTELEEMILESKPLHKKKRLAKKEDMKRKCDSSTQCLLQEHLDVSQKBEFI 360
Qy 361 IFNREKVNDRFNKPNLALEOTKDPQVTNGQ 392
Db 361 IFNREKVNDRFNKPNLALEOTKDPQGEDGQ 392
RESULT 7
ABG70700
ID ABG70700 standard; protein; 396 AA.
XX AC ABG70700;
XX DT 17-JAN-2003 (first entry)
XX DE Human serine/threonine protein kinase-like kinase.
XX KW Human; kinase; serine/threonine kinase; immune response; transgenic;
XX OS Homo sapiens.
XX FH Location/Qualifiers
FT Modified-site 2..7
FT Modified-site /label= N_myristoylation_site
FT Modified-site 4..7
FT Modified-site /label= N_glycosylation_site
FT Modified-site 5..7
FT Modified-site /label= Protein_kinase_C_phosphorylation_site
FT Modified-site 6..8
FT Binding-site /label= Protein_kinase_C_phosphorylation_site
FT Binding-site 29..52
FT Modified-site /label= Protein_kinase_ATP-binding_region
FT Modified-site 33..36
FT Modified-site /label= Casein_kinase_II_phosphorylation_site
FT Modified-site 43..46
FT Modified-site /label= N_glycosylation_site
FT Modified-site 45..47
FT Modified-site /label= Protein_kinase_C_phosphorylation_site
FT Modified-site 89..92
FT Modified-site /label= Casein_kinase_II_phosphorylation_site
FT Modified-site 122..124
FT Active-site /label= Protein_kinase_C_phosphorylation_site
FT Active-site 142..154
FT Modified-site /label= Serine/threonine_protein_kinase_active_site
FT Modified-site 193..195
FT Modified-site /label= Protein_kinase_C_phosphorylation_site
FT Modified-site 194..196
FT Modified-site /label= Protein_kinase_C_phosphorylation_site
FT Modified-site 197..202
FT Modified-site /label= N_myristoylation_site
FT Modified-site 212..215
FT Modified-site /label= Casein_kinase_II_phosphorylation_site
FT Modified-site 218..221
FT Modified-site /label= Amidation_site
FT Modified-site 230..233
FT Modified-site /label= Casein_kinase_II_phosphorylation_site
FT Modified-site 391..396
FT Modified-site /label= N_myristoylation_site
XX

PN 2002127683-A1.
XX 12-SEP-2002.
XX 09-MAR-2001; 2001US-00801876.
XX 09-MAR-2001; 2001US-00801876.
XX (YEJ)/ YE J.
XX (YANC)/ YAN C.
XX (DPR)/ DI FRANCESCO V.
XX (BEAS)/ BEASLEY E M.
PI Ye J, Yan C, Di Francesco V, Beasley EM;
XX WPI; 2003-028938/02.
DR N-PSDB; ABS55499, ABS55500.
PT Novel isolated human kinase peptide useful for treating disorder
PT characterized by absence of, in appropriate or unwanted expression of the
PT kinase protein, and as immunogens to raise antibodies.
XX Claim 1; Fig 2; 174pp; English.
XX The present invention relates to the isolation of a human kinase and the
XX polynucleotide sequences encoding it. The human kinase of the invention
XX is related to the serine/threonine kinase subfamily. The gene encoding
XX the human kinase is located on chromosome 5. The polypeptide and
XX polynucleotide sequences of the invention are useful for treating a
XX disease or condition mediated by a human kinase. Both the polypeptide and
XX polynucleotide sequences are useful as models for the development of
XX human therapeutics, for identifying therapeutic proteins, as targets for
XX development of human therapeutic agents, and as query sequences to
XX perform a search against sequence data bases to identify other family
XX members of related sequences. The polypeptide is useful to raise
XX antibodies or to elicit another immune response, as a reagent in assays
XX designed to quantitatively determine levels of the protein in biological
XX fluids, as markers for tissues in which the corresponding protein is
XX preferentially expressed, in drug screening assays, in cell-based or cell
XX -free systems, to identify compounds that modulate kinase activity of the
XX protein in its natural state, or an altered form that causes the specific
XX disease or pathology associated with the kinase, to screen a compound for
XX the ability to stimulate or inhibit interaction between the kinase
XX protein and a molecule that normally interacts with the kinase protein,
XX and in pharmacogenomic analysis. The polynucleotide is useful for
XX monitoring the effectiveness of modulating compounds on the expression or
XX activity of the human kinase gene in clinical trials or in a treatment
XX regimen, in diagnostic assays for qualitative changes in a human kinase
XX nucleic acid that leads to a pathology, for testing an individual for a
XX genotype that while not necessarily causing a disease, nevertheless
XX affects the treatment modality, as antisense constructs to control human
XX kinase gene expression in cells, tissues and organisms, for gene therapy
XX in patients containing cells that are aberrant in human kinase gene
XX expression, and to produce transgenic animals. The present sequence
XX represents a human kinase related to the serine/threonine protein kinase
XX subfamily
SQ Sequence 396 AA;

Query Match 95.2%; Score 2047; DB 6; Length 396;
Best Local Similarity 98.7%; Pred. No. 7.2e-186;
Matches 387; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Qy 1 MGANTSRKPPVPDENEDVNFDPHEILRAJGKSGFGKVCIVQKNDTKMYAMKYNKQKV 60
Db 1 MGANTSRKPPVPDENEDVNFDPHEILRAJGKSGFGKVCIVQKNDTKMYAMKYNKQKV 60
Qy 61 ERNEVRNVFKELQIMQGLEHPLVNLWYSFQDEDMFMVVDLLGLGDLRYHLQONVHFXE 120
Db 61 ERNEVRNVFKELQIMQGLEHPLVNLWYSFQDEDMFMVVDLLGLGDLRYHLQONVHFXE 120
Qy 121 ETVKLFICELVWALDYQNRHDMKPDNILLDEGHVHTDFAAAMLPREIQTITM 180

Db 121 ETVKLFICELVWALDYLNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTM 180
Qy 181 AGTKPYMAPENFSSRGAGYSFAVDWWSLGTAYAYELLGRPPYHIRSTSSKEIVHTFET 240
Db 181 AGTKPYMAPENFSSRGAGYSFAVDWWSLGTAYAYELLGRPPYHIRSTSSKEIVHTFET 240
Qy 241 TVVTYPSAWSQEMVSLKLLLEPNPDORFSDVQNFPPYNDINWDVAFQKRLIPGIP 300
Db 241 TVVTYPSAWSQEMVSLKLLLEPNPDORFSDVQNFPPYNDINWDVAFQKRLIPGIP 300
Qy 301 NKGRNLCDPTFELEEMILESPLHKKKRLAKKEDMRKCDSSQTCLLQEHLDVQKEFI 360
Db 301 NKGRNLCDPTFELEEMILESPLHKKKRLAKKEDMRKCDSSQTCLLQEHLDVQKEFI 360
Qy 361 IFNREKVNDRDNKQPNLALEQTKDPQVINGQ 392
Db 361 IFNREKVNDRDNKQPNLALEQTKDPQGEDGQ 392

RESULT 8
ABU62276
ID ABU62276 standard; protein; 396 AA.
AC ABU62276;
DT 01-SEP-2003 (first entry)
DE Human kinase.
XX Human; enzyme; kinase; gene therapy; cancer; inflammation; psoriasis;
KW arteriosclerosis.
XX Homo sapiens.
XX US2003027307-A1.
XX 06-FEB-2003.
XX 26-SEP-2002; 2002US-00254869.
XX 09-MAR-2001; 2001US-00801876.
XX (APPL-) APPLERA CORP.
XX Ye J, Yan C, Di Francesco V, Beasley EM;
XX WPI; 2003-492035/58.
XX N-PSDB; ACA62840, ACA62841.
XX New isolated human kinase proteins, useful for treating disorders
PT mediated by kinase pathway (e.g. cancers, inflammations, arteriosclerosis
PT or psoriasis), or for development of human therapeutics and diagnostic
PT compositions.
XX Claim 1; Fig 2A; 185pp; English.
XX The invention relates to a new isolated human kinase peptide. The human
CC kinase peptide and nucleic acid molecules are useful in the development
CC of human therapeutics and diagnostic compositions. The peptides are
CC useful for treating disorders (e.g. cancers, inflammations,
CC arteriosclerosis or psoriasis) characterised by an absence of,
CC inappropriate, or unwanted expression of the kinase protein. These
CC molecules are particularly useful as models for developing human
CC therapeutic targets, identifying therapeutic proteins, or serving as
CC targets for the development of human therapeutic agents that modulate
CC kinase activity in cells and tissues that express the kinase. The
CC peptides are also useful for raising antibodies or eliciting an immune
CC response; as a reagent (including the labelled reagent) in assays
CC designed to quantitatively determine levels of the protein (or its
CC binding partner or ligand) in biological fluids; or as markers for
CC tissues in which the corresponding protein is preferentially expressed.
CC The agents identified are useful for treating a subject with a disorder
CC mediated by kinase pathway. The present sequence represents the amino

CC acid sequence of a human kinase.
XX Sequence 396 AA;
SQ Query Match 95.2%; Score 2047; DB 6; Length 396;
Best/Local Similarity 98.7%; Pred. No. 7.2e-186;
Matches 387; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Qy 1 MGANTSRRKPVFDENEDVDFEILRAIGKSGFGKCIQKNDTKMYAMKYNKQKCV 60
Db 1 MGANTSRRKPVFDENEDVDFEILRAIGKSGFGKCIQKNDTKMYAMKYNKQKCV 60
Qy 61 ERNEVRNVFKEIQMOGLEHFFLVNLWYSQDEDMFVVDLLGGDLRYHLQNVHFK 120
Db 61 ERNEVRNVFKEIQMOGLEHFFLVNLWYSQDEDMFVVDLLGGDLRYHLQNVHFK 120
Qy 121 ETVKLFICELVWALDYLNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTM 180
Db 121 ETVKLFICELVWALDYLNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTM 180
Qy 181 AGTKPYMAPENFSSRGAGYSFAVDWWSLGTAYAYELLGRPPYHIRSTSSKEIVHTFET 240
Db 181 AGTKPYMAPENFSSRGAGYSFAVDWWSLGTAYAYELLGRPPYHIRSTSSKEIVHTFET 240
Qy 241 TVVTYPSAWSQEMVSLKLLLEPNPDORFSDVQNFPPYNDINWDVAFQKRLIPGIP 300
Db 241 TVVTYPSAWSQEMVSLKLLLEPNPDORFSDVQNFPPYNDINWDVAFQKRLIPGIP 300
Qy 301 NKGRNLCDPTFELEEMILESPLHKKKRLAKKEDMRKCDSSQTCLLQEHLDVQKEFI 360
Db 301 NKGRNLCDPTFELEEMILESPLHKKKRLAKKEDMRKCDSSQTCLLQEHLDVQKEFI 360
Qy 361 IFNREKVNDRDNKQPNLALEQTKDPQVINGQ 392
Db 361 IFNREKVNDRDNKQPNLALEQTKDPQGEDGQ 392

RESULT 9
ADL09162
ID ADL09162 standard; protein; 396 AA.
XX ADL09162;
XX 20-MAY-2004 (first entry)
DE Human protein kinase.
XX human; Kinase Modulator; serine/threonine protein kinase subfamily;
KW Gene Therapy; enzyme; protein kinase.
XX Homo sapiens.
XX US2004043466-A1.
XX 04-MAR-2004.
XX 23-SEP-2003; 2003US-00667442.
XX 09-MAR-2001; 2001US-00801876.
XX 26-SEP-2002; 2002US-00254869.
XX (APPL-) APPLERA CORP.
XX Ye J, Yan C, Di Francesco V, Beasley EM;
XX WPI; 2004-280746/26.
XX N-PSDB; ADL09161.
XX New isolated human kinase peptides, useful as models for developing human
PT therapeutic targets, aid in the identification of therapeutic proteins,
PT or for diagnosing, preventing and treating kinase-related conditions.
XX Claim 1; SEQ ID NO 2; 184pp; English.

XX The invention relates to new isolated human protein kinase polypeptide
 CC and polynucleotides. The new human kinase protein is related to the
 CC serine/threonine protein kinase subfamily. The kinase peptides and
 CC nucleic acid molecules are useful as models for the development of human
 CC therapeutic targets, aid in the identification of therapeutic proteins,
 CC and serve as targets for the development of human therapeutic agents that
 CC modulate kinase activity in cells and tissues that express the kinase.
 CC The peptides are also useful in the diagnosis, prevention and treatment
 CC of kinase-related conditions. The peptide may be used in drug screening
 CC assays, in assays to determine the biological activity of the protein, to
 CC raise antibodies or to elicit another immune response, as a reagent in
 CC assays designed to quantitatively determine levels of the protein in
 CC biological fluids, or as markers for tissues in which the corresponding
 CC protein is preferentially expressed. The antibodies are useful in
 CC pharmacogenomic analysis, for inhibiting protein function, or for tissue
 CC typing. The nucleic acid molecules are useful as probes, primers,
 CC chemical intermediates, or in biological assays. The present sequence
 CC represents the amino acid sequence of the isolated human protein kinase.
 XX Sequence 396 AA;

Query Match 95.2%; Score 2047; DB 8; Length 396;
 Best Local Similarity 98.7%; Pred No. 7.2e-186;
 Matches 397; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MGANTSRKPPVPDENEDVNFDFEILRAIGKSGFGKVCIVQKNDTKMYAMKMKQKCV 60
 Db 1 MGANTSRKPPVPDENEDVNFDFEILRAIGKSGFGKVCIVQKNDTKMYAMKMKQKCV 60
 QY 61 ERNEVRNVFKELQIMQGLEHPLVNLWYSFQDEEDMFVVDLLGGDLRYHLQQNVHFK 120
 Db 61 ERNEVRNVFKELQIMQGLEHPLVNLWYSFQDEEDMFVVDLLGGDLRYHLQQNVHFK 120
 QY 121 ETVKLFICELVMDLYLQNRILHRDKPDNILLDEHGHVHTDPIAAMLPRETQITTM 180
 Db 121 ETVKLFICELVMDLYLQNRILHRDKPDNILLDEHGHVHTDPIAAMLPRETQITTM 180
 QY 181 AGTKPYMAPFSSRKAGYGFVDMWSLGVTVAYELLGRRPYHRSSTSKSKEIVHTFET 240
 Db 181 AGTKPYMAPFSSRKAGYGFVDMWSLGVTVAYELLGRRPYHRSSTSKSKEIVHTFET 240
 QY 241 TVVTYPSAWSQBMVSLKKLEPNPDORFQSDVQNFPPYNDINWDVAFQKRLIPGIP 300
 Db 241 TVVTYPSAWSQBMVSLKKLEPNPDORFQSDVQNFPPYNDINWDVAFQKRLIPGIP 300
 QY 301 NKGRNLNCDPTFELEEMILESPLHKKKRLAKKEDMKKCDSSOTCLLOEHLDSVQKEFI 360
 Db 301 NKGRNLNCDPTFELEEMILESPLHKKKRLAKKEDMKKCDSSOTCLLOEHLDSVQKEFI 360
 QY 361 IFNREKVRNDRNKPQNLALBQTKDPQVNTNGQ 392
 Db 361 IFNREKVRNDRNKPQNLALBQTKDPQVNTNGQ 392

RESULT 10

ID ADF44523 standard; protein; 398 AA.
 XX ADF44523;
 AC ADF44523;

DT 12-FEB-2004 (first entry)
 XX

DE Mouse kinase protein SEQ ID NO:41.
 XX

KW cytotatic; nootropic; neuroprotective; antidiabetic; screening;
 KW regulation; drug development; protein-associated disease; cancer;
 KW dementia; diabetes; kinase; enzyme; mouse.
 XX

OS Mus musculus.
 XX

XX WO2003084992-A1.
 XX

PD 16-OCT-2003.
 XX

XX 04-APR-2003; 2003WO-JP004330.
 XX

XX 05-APR-2002; 2002JP-00103396.
 PR

PR 23-APR-2002; 2002JP-00120904.
 PR

PR 02-MAY-2002; 2002JP-00130601.
 PR

XX 04-DEC-2002; 2002JP-00352520.
 XX

PA (RIKE) RIKEN KK.
 PA

PA (DNAP-) DNAFORM KK.
 PA

XX (MITU) MITSUBISHI CHEM CORP.
 XX

Hayashizaki Y, Kamiya M, Kubodera H, Watanabe W;
 WPI; 2003-833568/77.

DR N-FSDB; ADF44497.
 XX

PT Proteins and encoded DNAs with kinase activity, useful in screening
 PT substances for regulating such activity and in developing drugs for the
 PT protein-associated diseases e.g. cancer, dementia and diabetes.
 XX

XX Claim 1; SEQ ID NO 41; 342pp; Japanese.
 PS

XX The present invention describes a protein: (a) containing any of the
 CC amino acid sequences of ADF44509 to ADF44534 or ADF44544; or (b) based on
 CC any of the sequences in (a) but with some amino acids deleted,
 CC substituted and/or added and having kinase activity. Also described: (1)
 CC a DNA encoding any of the proteins; (2) a full-length cDNA encoding the
 CC protein; (3) a DNA which is: (a) a DNA containing any of the base
 CC sequences in ADF44483 to ADF44508 or ADF44543; (b) a DNA derived from any
 CC of the sequences in (a) but with some bases deleted, substituted and/or
 CC added and encoding a protein with kinase activity; or (c) a DNA
 CC hybridisable with any of the sequences in (a) or their complementary
 CC strands under stringent conditions and encoding a protein with kinase
 CC activity; (4) a recombinant vector containing the DNA; (5) a cell
 CC transfected with the DNA or recombinant vector, or an individual produced
 CC from the cell; (6) recombinant proteins produced by such cells; (7) an
 CC oligonucleotide containing 5-10 consecutive bases in any of the base
 CC sequences, its sense oligonucleotide, an antisense oligonucleotide with a
 CC complementary strand of such sense oligonucleotide, or an oligonucleotide
 CC derivative of the (anti-)sense oligonucleotide; (8) an antibody
 CC specifically binding to the protein, or its partial fragment; (9) a
 CC method for screening substances for regulating activity of the protein by
 CC contacting a test substance with such protein before measuring changes in
 CC the protein activity due to the test substance; (10) a method for
 CC screening substances regulating expression of the DNA by contacting a
 CC test substance with cells transfected with the gene and detecting changes
 CC in expression level of the DNA in such cells; (11) recordable media for
 CC reading in a computer with information on the amino acid sequences of the
 CC proteins, and/or base sequences of the DNAs stored; and (12) a support
 CC for binding with any of the proteins and/or DNAs. The proteins and their
 CC encoded DNAs have cytostatic, nootropic, neuroprotective and antidiabetic
 CC activities. They can be used in screening substances for regulating such
 CC activity and in developing drugs for the protein-associated diseases e.g.
 CC cancer, dementia and diabetes. The present sequence is used in the
 CC exemplification of the present invention.
 XX

SQ Sequence 398 AA;

Query Match 87.4%; Score 1880; DB 7; Length 398;
 Best Local Similarity 91.2%; Pred. No. 5.8e-170;
 Matches 351; Conservative 20; Mismatches 14; Indels 0; Gaps 0;

QY 1 MGANTSRKPPVPDENEDVNFDFEILRAIGKSGFGKVCIVQKNDTKMYAMKMKQKCV 60

Db 1 MGANTSRKPPVPDENEDVNFDFEILRAIGKSGFGKVCIVQKNDTKMYAMKMKQKCV 60

QY 61 ERNEVRNVFKELQIMQGLEHPLVNLWYSFQDEEDMFVVDLLGGDLRYHLQQNVHFK 120

Db 61 ERNEVRNVFKELQIMQGLEHPLVNLWYSFQDEEDMFVVDLLGGDLRYHLQQNVHFK 120

QY 121 ETVKLFICELVMDLYLQNRILHRDKPDNILLDEHGHVHTDPIAAMLPRETQITTM 180

Db 121 DTVKLFICELAMALDYLSQRIIHRDMKPDNILLDEHGHVHTDFNIAMLPKETRTTV 180
 Qy 181 AGTPYMAPEMFSSRGAGYSFAVDWMSLGVATYELLGRPPYHRSSTSSKEIVHTFET 240
 Db 181 AGTPYMAPEMFTSRKETGYSFAVDWMSLGVATYELLGRPPYHRSSTSSKEIVNNFET 240
 Qy 241 TVVTYPSAWSQEMVSLKLLLEPNPDORFESQSDVQNFPPYMDINWDVAFQKRLIPGIP 300
 Db 241 AIVTYPYSAWSQEMVSLKLLLEPNPDORFESQSDVQNFPPYMDINWDVAFQKRLIPGIP 300
 Qy 301 NKGRNLCDPTPELEEMILESPLHKKKRLAKKEMKCDSSQTCLLQHLDSVQKEFI 360
 Db 301 TKGRNLCDPTPELEEMILESPLHKKKRLAKKEMKCDSSQTCLLQHLDSVQKEFI 360
 Qy 361 IFNREKVNDRPNKQPNLALEQTKD 385
 Db 361 IFNREKVKDFNQANLALEQTKN 385

RESULT 11

ADP44527
ID ADP44527 standard; protein; 398 AA.

XX AC ADP44527;

DT 12-FEB-2004 (first entry)

XX DE Mouse kinase protein SEQ ID NO:45.

XX KW cytostatic; nontropic; neuroprotective; antidiabetic; screening;
 KW regulation; drug development; protein-associated disease; cancer;
 KW dementia; diabetes; kinase; enzyme; mouse.

XX OS Mus musculus.

XX PN WO2003084992-A1.

XX PD 16-OCT-2003.

XX PF 04-APR-2003; 2003WO-JP004330.

XX PR 05-APR-2002; 2002JP-00103396.

XX PR 23-APR-2002; 2002JP-00120904.

XX PR 02-MAY-2002; 2002JP-00130601.

XX PR 04-DEC-2002; 2002JP-00325250.

XX PA (RIKE) RIKEN KK.

XX PA (DNAP-) DNAFORM KK.

XX PA (MITU) MITSUBISHI CHEM CORP.

XX PI Hayashizaki Y, Kamiya M, Kubodera H, Watanabe W;

XX DR WPI; 2003-833568/77.

XX DR N-PSDB; ADP44501.

XX PS Claim 1; SEQ ID NO 45; 342pp; Japanese.

CC The present invention describes a protein: (a) containing any of the
 CC amino acid sequences of ADP44509 to ADP44534 or ADP44544; or (b) based on
 CC any of the sequences in (a) but with some amino acids deleted.
 CC substituted and/or added and having kinase activity. Also described: (1)
 CC a DNA encoding any of the proteins; (2) a full-length cDNA encoding the
 CC protein; (3) a DNA which is: (a) a DNA containing any of the base
 CC sequences in ADP44483 to ADP44508 or ADP44543; (b) a DNA derived from any
 CC of the sequences in (a) but with some bases deleted, substituted and/or
 CC added and encoding a protein with kinase activity; or (c) a DNA
 CC hybridisable with any of the sequences in (a) or their complementary
 CC strands under stringent conditions and encoding a protein with kinase

CC activity; (4) a recombinant vector containing the DNA; (5) a cell
 CC transferred with the DNA or recombinant vector, or an individual produced
 CC from the cell; (6) recombinant proteins produced by such cells; (7) an
 CC oligonucleotide containing 5-10 consecutive bases in any of the base
 CC sequences, its sense oligonucleotide, an antisense oligonucleotide with a
 CC complementary strand of such sense oligonucleotide, or an oligonucleotide
 CC derivative of the (anti-)sense oligonucleotide; (8) an antibody
 CC specifically binding to the protein, or its partial fragment; (9) a
 CC method for screening substances for regulating activity of the protein by
 CC contacting a test substance with such protein before measuring changes in
 CC the protein activity due to the test substance; (10) a method for
 CC screening substances regulating expression of the DNA by contacting a
 CC test substance with cells transfected with the gene and detecting changes
 CC in expression level of the DNA in such cells; (11) recordable media for
 CC reading in a computer with information on the amino acid sequences of the
 CC proteins, and/or base sequences of the DNAs stored; and (12) a support
 CC for binding with any of the proteins and/or DNAs. The proteins and their
 CC encoded DNAs have cytostatic, nontropic, neuroprotective and antidiabetic
 CC activities. They can be used in screening substances for regulating such
 CC activity and in developing drugs for the protein-associated diseases e.g.
 CC cancer, dementia and diabetes. The present sequence is used in the
 CC exemplification of the present invention.

XX SQ Sequence 398 AA;

Query Match 87.2%; Score 1875; DB 7; Length 398;

Best Local Similarity 90.9%; Pred. No. 1.7e-169;

Matches 350; Conservative 21; Mismatches 14; Indels 0; Gaps 0;

Qy 1 MGANTSRKPPVFDENEDVNFDFEILRAIGKSGFGKVICIVQKNDTKQYAMKYNKQKCV 60

Db 1 MGANTSKAPVFDENEDVNFDFEILRAIGKSGFGKVICIVQKNDTKQYAMKYNKQKCV 60

Qy 61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEDMFMVVDLLGGDLRYHLQONVHFE 120

Db 61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEDMFMVVDLLGGDLRYHLQONVHFE 120

Qy 121 ETVKLFICELVMDLYLQONRIIHRDMKPDNILLDEHGHVHTDFNIAMLPRETQITTM 180

Db 121 DTVKLFICELAMALDYLSQRIIHRDMKPDNILLDEHGHVHTDFNIAMLPKETRTTV 180

Qy 181 AGTKPYMAPEMFSSRGAGYSFAVDWMSLGVATYELLGRPPYHRSSTSSKEIVHTFET 240

Db 181 AGTKPYMAPEMFTSRKETGYSFAVDWMSLGVATYELLGRPPYHRSSTSSKEIVNNFET 240

Qy 241 TVVTYPSAWSQEMVSLKLLLEPNPDORFESQSDVQNFPPYMDINWDVAFQKRLIPGIP 300

Db 241 AIVTYPYSAWSQEMVSLKLLLEPNPDORFESQSDVQNFPPYMDINWDVAFQKRLIPGIP 300

Qy 301 NKGRNLCDPTPELEEMILESPLHKKKRLAKKEMKCDSSQTCLLQHLDSVQKEFI 360

Db 301 TKGRNLCDPTPELEEMILESPLHKKKRLAKKEMKCDSSQTCLLQHLDSVQKEFI 360

Qy 361 IFNREKVNDRPNKQPNLALEQTKD 385

Db 361 IFNREKVKDFNQANLALEQTKN 385

RESULT 12

ADMO3989

ID ADMO3989 standard; protein; 358 AA.

XX AC ADMO3989;

XX DT 20-MAY-2004 (first entry)

XX DE Human protein of the invention SEQ ID NO:2674.

XX KW human; gene therapy; diagnostic marker; pharmaceutical.

XX OS Homo sapiens.

XX PN EP1347046-A1.

XX 24-SEP-2003.
PD 12-APR-2002; 2002EP-00008400.
XX PF
XX PR
XX PR
XX (REAS-) RES ASSOC BIOTECHNOLOGY.
XX Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
XX WPI: 2003-723358/69.
DR N-PSDB; ADM01546.
XX
PT New polynucleotides and polypeptides are useful in gene therapy, for
PT developing a diagnostic marker or medicines for regulating their
PT expression and activity, or as a target of gene therapy.
XX
PS Claim 1; SEQ ID NO 2674; 305pp; English.
XX
CC The invention relates to a novel human polynucleotide and the encoded
CC polypeptide. A polynucleotide of the invention may have a use in gene
CC therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful
CC as a primer for synthesizing the polynucleotide or as a probe for
CC detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are
CC useful in gene therapy, for developing a diagnostic marker or medicines
CC for regulating their expression and activity, or as a target of gene
CC therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides
CC are useful as pharmaceutical agents. The present sequence represents a
CC protein sequence of the invention.
XX
SQ Sequence 358 AA;
Query Match 84.9%; Score 1827; DB 7; Length 358;
Best Local Similarity 100.0%; Pred. No. 5.6e-165;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGANTSRRPPVDFDENEDVNFDFELRLAIGKSGFGKVCIVQNDTKMYAMKYNKQKCV 60
DB 1 MGANTSRRPPVDFDENEDVNFDFELRLAIGKSGFGKVCIVQNDTKMYAMKYNKQKCV 60
QY 61 ERNEVRNVFKELIQMOGLEHPFLVNLWYSFQDEDMFVVDLLGGDLRYHLQNVHPKE 120
DB 61 ERNEVRNVFKELIQMOGLEHPFLVNLWYSFQDEDMFVVDLLGGDLRYHLQNVHPKE 120
QY 121 ETVKLFICELVMDLYLQNRQRIHRDMKPDNILLDEHGHVHTDFTNIAAMLPRETQITTM 180
DB 121 ETVKLFICELVMDLYLQNRQRIHRDMKPDNILLDEHGHVHTDFTNIAAMLPRETQITTM 180
QY 181 AGTKPYMAPEMFSSRRKGAGYFAVDWWSLGVTA YELLGRPPHYHRSSTSSKEIVHTPET 240
DB 181 AGTKPYMAPEMFSSRRKGAGYFAVDWWSLGVTA YELLGRPPHYHRSSTSSKEIVHTPET 240
QY 241 TVVTYPSAWSQBMVSLKLLKLEPNPDRFSQSDVQNFYPMNDINWDAVFQKRLIPGIP 300
DB 241 TVVTYPSAWSQBMVSLKLLKLEPNPDRFSQSDVQNFYPMNDINWDAVFQKRLIPGIP 300
QY 301 NKGRLNCDPFTFELEEMILESPLHKKKRLAKKXKMDKCDSSQ 344
DB 301 NKGRLNCDPFTFELEEMILESPLHKKKRLAKKXKMDKCDSSQ 344
RESULT 13
AAU03504
ID AAU03504 standard; protein; 327 AA.
XX
XX AAU03504;
XX
DT 12-SEP-2001 (first entry)
XX
DE Human protein kinase #4.

XX Human; protein kinase; PTK; STK; cancer; cardiovascular disease;
KW metabolic disorder; immune related disease; neurological disorder;
KW neurodegenerative disorder; inflammatory disorder; infectious disease;
KW reproductive disorder.
XX Homo sapiens.
OS
XX W0200138503-A2.
FN
XX 31-MAY-2001.
PD
XX 22-NOV-2000; 2000WO-US032085.
PF
XX 24-NOV-1999; 99US-0167482P.
PR
XX (SUGE-) SUGEN INC.
PA
XX Plowman GD, Whyte D, Manning G, Sudarsanam S, Martinez R;
PI Flanagan P, Clary D;
PI
XX WPI: 2001-343950/36.
DR N-PSDB; AAS06704.
XX
CC Nucleic acids encoding human kinase polypeptides, useful for preventing
CC diagnosing and/or treating e.g. cancer, immune, cardiovascular and
CC neuronal-associated diseases, and microbial infections.
PT
PS Claim 7; Fig 2; 433pp; English.
XX
CC AAU03501-AAU03557 represent novel human protein kinases #1-57. The novel
CC protein kinases have been identified as members of the tyrosine or
CC serine/threonine kinase (PTK and STK) families. The polynucleotides
CC encoding protein kinases and the polypeptides may be used in the
CC prevention, diagnosis and treatment of diseases associated with
CC inappropriate kinase expression. For example, they may be used to treat
CC cancers (especially cancers of haematopoietic origin), cardiovascular
CC disease (e.g. atherosclerosis), metabolic disorders (e.g. diabetes),
CC immune related diseases (e.g. rheumatoid arthritis), neurological
CC disorders (e.g. schizophrenia), neurodegenerative disorders (e.g.
CC Parkinson's disease), inflammatory disorders (e.g. asthma), infectious
CC disease (e.g. HIV) and reproductive disorders (e.g. infertility).
CC Additionally, polynucleotides encoding protein kinases may be used for
CC gene therapy and as DNA probes in diagnostic assays. The protein kinase
CC polypeptides may be used as antigens in the production of antibodies
CC against the protein kinases and in assays to identify modulators of
CC protein kinase expression and activity
XX
SQ Sequence 327 AA;

Query Match 70.4%; Score 1513.5; DB 4; Length 327;
Best Local Similarity 87.6%; Pred. No. 3.5e-135;
Matches 297; Conservative 5; Mismatches 18; Indels 19; Gaps 4;
QY 1 MGANTSRRPPVDFDENEDVNFDFELRLAIGKSGFGKVCIVQNDTKMYAMKYNKQKCV 60
DB 1 MGANTSRRPPVDFDENEDVNFDFELRLAIGKSGFGKVCIVQNDTKMYAMKYNKQKCV 60
QY 61 ERNEVRNVFKELIQMOGLEHPFLVNLWYSFQDEDMFVVDLLGGDLRYHLQNVHPKE 120
DB 61 ERNEVRNVFKELIQMOGLEHPFLVNLWYSFQDEDMFVVDLLGGDLRYHLQNVHPKE 120
QY 121 ETVKLFICELVMDLYLQNRQRIHRDMKPDNILLDEHGHVHTDFTNIAAMLPRETQITTM 180
DB 121 ETVKLFICELVMDLYLQNRQRIHRDMKPDNILLDEHGHVHTDFTNIAAMLPRETQITTM 180
QY 181 AGTKPYMAPEMFSSRRKGAGYFAVDWWSLGVTA YELLGRPPHYHRSSTSSKEIVHTPET 240
DB 181 AGTKPYMAPEMFSSRRKGAGYFAVDWWSLGVTA YELLGRPPHYHRSSTSSKEIVHTPET 240
QY 241 TVVTYPSAWSQBMVSLKLLKLEPNPDRFSQSDVQNFYPMNDINWDAVFQKRLIPGIP 293
DB 241 TVVTYPSAWSQBMVSLKLLKLEPNPDRFSQSDVQNFYPMNDINWDAVFQKRLIPGIP 293
DE Human protein kinase #4.

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 17, 2004, 09:25:19 ; Search time 21 Seconds
(without alignments)
1285.306 Million cell updates/sec

Title: US-10-620-845-9

Perfect score: 2151

Sequence: 1 MGANTSRRKPPVFEDNEVDNF.....VTNGQMDTGLSEFTQTSKVS 407

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2151	100.0	407	4	US-09-841-683-9
2	2060	95.8	396	4	US-09-841-683-11
3	2047	95.2	396	4	US-09-801-876B-2
4	2047	95.2	396	4	US-10-254-869-2
5	1430.5	66.5	404	4	US-09-801-876B-4
6	1430.5	66.5	404	4	US-10-254-869-4
7	1423.5	66.2	403	4	US-09-801-876B-5
8	1423.5	66.2	403	4	US-10-254-869-5
9	1332.5	61.9	419	4	US-09-799-875-14
10	1328.5	61.8	384	4	US-09-801-876B-6
11	1328.5	61.8	384	4	US-10-254-869-6
12	1294.5	60.2	399	4	US-09-819-607-4
13	1174	54.6	236	4	US-09-841-683-7
14	1171	54.4	225	4	US-09-841-683-5
15	1142	53.1	369	4	US-09-819-607-2
16	1127.5	52.4	368	4	US-09-819-607-5
17	995.5	46.3	316	4	US-09-801-876B-7
18	995.5	46.3	316	4	US-10-254-869-7
19	852.5	39.6	347	4	US-09-801-876B-8
20	852.5	39.6	347	4	US-10-254-869-8
21	525	24.4	470	4	US-09-248-796A-18482
22	514.5	23.9	740	4	US-09-538-092-1178
23	509.5	23.7	336	4	US-09-394-455-2
24	509.5	23.7	343	4	US-09-394-455-15
25	509.5	23.7	343	4	US-09-394-455-34
26	509.5	23.7	350	4	US-09-538-092-946
27	509.5	23.7	351	4	US-09-394-455-4

Sequence 2, Appli
Sequence 501, App
Sequence 38, Appl
Sequence 6, Appli
Sequence 69, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 991, App
Sequence 1054, Ap
Sequence 20, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 8, Appli
Sequence 7, Appli
Sequence 20519, A
Sequence 6, Appli

28 508.5 23.6 587 1 US-08-313-274-2
29 504.5 23.5 398 4 US-09-538-092-501
30 503.5 23.4 343 4 US-09-394-455-38
31 503.5 23.4 350 3 US-09-457-040B-37
32 503.5 23.4 351 3 US-09-457-040B-6
33 503.5 23.4 595 4 US-09-417-197-69
34 498.5 23.2 689 1 US-08-221-817-18
35 498.5 23.2 689 1 US-08-454-439-18
36 498.5 23.2 689 5 PCT-US94-10487-18
37 497.5 23.1 350 4 US-09-538-092-991
38 495.5 23.0 481 4 US-09-538-092-1054
39 485.5 22.6 699 1 US-08-221-817-20
40 485.5 22.6 699 1 US-08-454-439-20
41 485.5 22.6 699 5 PCT-US94-10487-20
42 485 22.5 260 2 US-07-857-224B-8
43 484 22.5 260 2 US-07-857-224B-7
44 484 22.5 403 4 US-09-248-796A-20519
45 483 22.5 480 4 US-09-590-740-6

ALIGNMENTS

RESULT 1

US-09-841-683-9

; Sequence 9, Application US/09841683

; Patent No. 6617147

; GENERAL INFORMATION:

; APPLICANT: Hu, Yi

; APPLICANT: Nepomnichy, Boris

; APPLICANT: Wang, Xiaoming

; APPLICANT: Donoho, Gregory

; APPLICANT: Scoville, John

; APPLICANT: Walke, D. Wade

; TITLE OF INVENTION: No. 6617147el Human Kinase Proteins and Polynucleotides Encoding

; FILE REFERENCE: LEX-0167-USA

; CURRENT APPLICATION NUMBER: US/09/841,683

; PRIOR FILING DATE: 2001-04-24

; PRIOR APPLICATION NUMBER: US 60/199,499

; PRIOR FILING DATE: 2000-04-25

; PRIOR APPLICATION NUMBER: US 60/201,227

; PRIOR FILING DATE: 2000-05-01

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 9

; LENGTH: 407

; TYPE: PRT

; ORGANISM: homo sapiens

US-09-841-683-9

Query Match 100.0%; Score 2151; DB 4; Length 407;

Best Local Similarity 100.0%; Pred. No. 1.7e-197;

Matches 407; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MGANTSRRKPPVFEDNEVDNFHEILRAIGKSGFKVCIQKNDTKMYAMKYNKQKV	60
Db	1	MGANTSRRKPPVFEDNEVDNFHEILRAIGKSGFKVCIQKNDTKMYAMKYNKQKV	60
Qy	61	ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEEDMEFVVDLLGLGDLRYHLQNVHPKE	120
Db	61	ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEEDMEFVVDLLGLGDLRYHLQNVHPKE	120
Qy	121	ETVKLFTCELVMDYLNQRIIHRDMKPNILLDEHGHVHTDFTNIAAMLPRETQITTM	180
Db	121	ETVKLFTCELVMDYLNQRIIHRDMKPNILLDEHGHVHTDFTNIAAMLPRETQITTM	180
Qy	181	AGTKPYNAPEMFSSRRKAGYSFAVDWVSLGVTAYELLGRPPYHIRSTSSKEIVHVFET	240
Db	181	AGTKPYNAPEMFSSRRKAGYSFAVDWVSLGVTAYELLGRPPYHIRSTSSKEIVHVFET	240
Qy	241	TVVTYPSAWSOEYMSLLKLEPNPDORFQSDVQNFPPYMNNDINWDAVFQKRLIPGFI	300
Db	241	TVVTYPSAWSOEYMSLLKLEPNPDORFQSDVQNFPPYMNNDINWDAVFQKRLIPGFI	300

QY 301 NKGRNCPTTPELEEMILESPLHKKKKRLAKKEDMRKCDSSQTCCLQEHLDSSVQKEFI 360
Db 301 NKGRNCPTTPELEEMILESPLHKKKKRLAKKEDMRKCDSSQTCCLQEHLDSSVQKEFI 360
QY 361 IFNREKVNDRFNKQPNLALQEQTKDPQVINGQMDTGLSETFQTSKVS 407
Db 361 IFNREKVNDRFNKQPNLALQEQTKDPQVINGQMDTGLSETFQTSKVS 407

RESULT 2

US-09-841-683-11
; Sequence 11, Application US/09841683
; Patent No. 6617147
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Nepomnichy, Boris
; APPLICANT: Wang, Xiaoming
; APPLICANT: Donoho, Gregory
; APPLICANT: Scoville, John
; APPLICANT: Walke, D. Wade
; FILE REFERENCE: LEX-0167-USA
; TITLE OF INVENTION: No. 6617147el Human Kinase Proteins and Polynucleotides Encoding
; CURRENT APPLICATION NUMBER: US/09/841,683
; CURRENT FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: US 60/199,499
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US 60/201,227
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-841-683-11

Query Match 95.8%; Score 2060; DB 4; Length 396;
Best Local Similarity 99.2%; Pred. No. 8.5e-189;
Matches 389; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGANTSRRKPPVFDENEDVNFDFEILRAIGKSGFKVCIVQKNDTKKQYAMKYNKQKCV 60
Db 1 MGANTSRRKPPVFDENEDVNFDFEILRAIGKSGFKVCIVQKNDTKKQYAMKYNKQKCV 60
QY 61 ERNEVRNVFKELQIMQGLEHPEFLVNLWYSFQDEEDMFVVDLLGGDLRYHLOQNVHFK 120
Db 61 ERNEVRNVFKELQIMQGLEHPEFLVNLWYSFQDEEDMFVVDLLGGDLRYHLOQNVHFK 120
QY 121 ETVKLFICELVMDLYLQNRRIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTM 180
Db 121 ETVKLFICELVMDLYLQNRRIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTM 180
QY 181 AGTKPYMAPFSSRRKAGYSFAVDWWSLGVTVAYELLGRPRPHIRSTSSKEIVHTFET 240
Db 181 AGTKPYMAPFSSRRKAGYSFAVDWWSLGVTVAYELLGRPRPHIRSTSSKEIVHTFET 240
QY 241 TVVTYPSAWSQEMVSLKLLKLEPNPDRFSQSDVQNFPPYMDINWDVAFQKRLIPGFIP 300
Db 241 TVVTYPSAWSQEMVSLKLLKLEPNPDRFSQSDVQNFPPYMDINWDVAFQKRLIPGFIP 300
QY 301 NKGRNCPTTPELEEMILESPLHKKKKRLAKKEDMRKCDSSQTCCLQEHLDSSVQKEFI 360
Db 301 NKGRNCPTTPELEEMILESPLHKKKKRLAKKEDMRKCDSSQTCCLQEHLDSSVQKEFI 360
QY 361 IFNREKVNDRFNKQPNLALQEQTKDPQVINGQ 392
Db 361 IFNREKVNDRFNKQPNLALQEQTKDPQGEDGQ 392

RESULT 3

US-09-801-876B-2
; Sequence 2, Application US/09801876B

; Patent No. 6492155
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001160
; CURRENT APPLICATION NUMBER: US/09/801,876B
; CURRENT FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Human
US-09-801-876B-2

Query Match 95.2%; Score 2047; DB 4; Length 396;
Best Local Similarity 98.7%; Pred. No. 1.5e-187;
Matches 387; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGANTSRRKPPVFDENEDVNFDFEILRAIGKSGFKVCIVQKNDTKKQYAMKYNKQKCV 60
Db 1 MGANTSRRKPPVFDENEDVNFDFEILRAIGKSGFKVCIVQKNDTKKQYAMKYNKQKCV 60
QY 61 ERNEVRNVFKELQIMQGLEHPEFLVNLWYSFQDEEDMFVVDLLGGDLRYHLOQNVHFK 120
Db 61 ERNEVRNVFKELQIMQGLEHPEFLVNLWYSFQDEEDMFVVDLLGGDLRYHLOQNVHFK 120
QY 121 ETVKLFICELVMDLYLQNRRIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTM 180
Db 121 ETVKLFICELVMDLYLQNRRIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTM 180
QY 181 AGTKPYMAPFSSRRKAGYSFAVDWWSLGVTVAYELLGRPRPHIRSTSSKEIVHTFET 240
Db 181 AGTKPYMAPFSSRRKAGYSFAVDWWSLGVTVAYELLGRPRPHIRSTSSKEIVHTFET 240
QY 241 TVVTYPSAWSQEMVSLKLLKLEPNPDRFSQSDVQNFPPYMDINWDVAFQKRLIPGFIP 300
Db 241 TVVTYPSAWSQEMVSLKLLKLEPNPDRFSQSDVQNFPPYMDINWDVAFQKRLIPGFIP 300
QY 301 NKGRNCPTTPELEEMILESPLHKKKKRLAKKEDMRKCDSSQTCCLQEHLDSSVQKEFI 360
Db 301 NKGRNCPTTPELEEMILESPLHKKKKRLAKKEDMRKCDSSQTCCLQEHLDSSVQKEFI 360
QY 361 IFNREKVNDRFNKQPNLALQEQTKDPQVINGQ 392
Db 361 IFNREKVNDRFNKQPNLALQEQTKDPQGEDGQ 392

RESULT 4

US-10-254-869-2
; Sequence 2, Application US/10254869
; Patent No. 6653117
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001160DIV
; CURRENT APPLICATION NUMBER: US/10/254,869
; CURRENT FILING DATE: 2002-09-26
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Human
US-10-254-869-2

Query Match 95.2%; Score 2047; DB 4; Length 396;
Best Local Similarity 98.7%; Pred. No. 1.5e-187;
Matches 387; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGANTSRRKPPVFDENEDVNFDPHFILRAIGKSGFGKVCIVQKNDTKKMYAMKYNKQCV 60
DB 1 MGANTSRRKPPVFDENEDVNFDPHFILRAIGKSGFGKVCIVQKNDTKKMYAMKYNKQCV 60
QY 61 ERNEVRNVFKELQIMOGLEHPFLVNLWYSFQDEEDFMVVDLLGGDLRYHLQONVHFK 120
DB 61 ERNEVRNVFKELQIMOGLEHPFLVNLWYSFQDEEDFMVVDLLGGDLRYHLQONVHFK 120
QY 121 ETVKLFICELVMDLYLQNRHIDMKPDNILLDEGHVHITDFNIAAMLPRETOITTT 180
DB 121 ETVKLFICELVMDLYLQNRHIDMKPDNILLDEGHVHITDFNIAAMLPRETOITTT 180
QY 181 AGTKPYMAPFSSRKAGYSFAVDWMSLGTAYELLGRPRPYHRSSTSSKEIVHTFET 240
DB 181 AGTKPYMAPFSSRKAGYSFAVDWMSLGTAYELLGRPRPYHRSSTSSKEIVHTFET 240
QY 241 TVVTYPSAWSQEWVSLKLLKLEPNPDQRFQSDVQNFPMYNDINWDAVFKRLIPGIP 300
DB 241 TVVTYPSAWSQEWVSLKLLKLEPNPDQRFQSDVQNFPMYNDINWDAVFKRLIPGIP 300
QY 301 NGRNLCDPTFELEEMILESKPLHKKKRLAKKEKDMRKCDSSOTCLLOHLSVQKEFI 360
DB 301 NGRNLCDPTFELEEMILESKPLHKKKRLAKKEKDMRKCDSSOTCLLOHLSVQKEFI 360
QY 361 IFNREKVNRFNKRQPNLALQTKDPQVTNGQ 392
DB 361 IFNREKVNRFNKRQPNLALQTKDPQVTNGQ 392

RESULT 5
US-09-801-876B-4
; Sequence 4, Application US/09801876B
; Patent No. 6492155
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001160
; CURRENT FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 404
; TYPE: PRT
; ORGANISM: Mus Musculus
US-09-801-876B-4

Query Match 66.5%; Score 1430.5; DB 4; Length 404;
Best Local Similarity 68.1%; Pred. No. 1.6e-128;
Matches 280; Conservative 43; Mismatches 71; Indels 17; Gaps 5;
QY 1 MGANTSRRKPPVFDENEDVNFDPHFILRAIGKSGFGKVCIVQKNDTKKMYAMKYNKQCV 60
DB 1 MGNHSHKPPVFDENEVNFDFHQLRAIGKSGFGKVCIVQKNDTKKMYAMKYNKQCV 60
QY 61 -ERNEVRNVFKELQIMOGLEHPFLVNLWYSFQDEEDFMVVDLLGGDLRYHLQONVHFK 119
DB 61 QERDEVNRFRELQIMOGLEHPFLVNLWYSFQDEEDFMVVDLLGGDLRYHLQONVHFT 120
QY 120 EETVKLFICELVMDLYLQNRHIDMKPDNILLDEGHVHITDFNIAAMLPRETOITTT 179
DB 121 EGTVKLYICELALALEYLQRYHIIHRDIPDNILLDEGHVHITDFNIAATVLSKSEKASS 180
QY 180 MAGTKPYMAPFSSRKAGYSFAVDWMSLGTAYELLGRPRPYHRSSTSSKEIVHT 237
DB 181 MAGTKPYMAPFSSRKAGYSFAVDWMSLGTAYELLGRPRPYHRSATPIDEILNM 240
QY 238 FETTVVTPSAWSQEWVSLKLLKLEPNPDQRFQSDVQNFPMYNDINWDAVFKRLIPG 297
DB 241 FKVERVHYSTWCEGMVSLKLLKLTQDPESRLSLRDIQSWTYLADNWDNDAVFEKALMPG 300
QY 357 KEFIIIFNREKVNRFNKRQPNLALQTKDPQVT--NQMDTGLSETFQTSK 405
DB 361 KEFIIIFNREKLR-----QQGHGQSLDLDGRIGSQTSKLDQGR 400

RESULT 7
US-09-801-876B-5
; Sequence 5, Application US/09801876B
; Patent No. 6492155
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001160

QY 298 FPNKGRNLCDPTFELEEMILESKPLHKKKRLAK-KEKDMRKCDSSOTCLLOHLSVQ 356
DB 301 FPNKGRNLCDPTFELEEMILESKPLHKKKRLAKHRSRSTKDCSPLNGHLOQCLETVR 360
QY 357 KEFIIIFNREKVNRFNKRQPNLALQTKDPQVT--NQMDTGLSETFQTSK 405
DB 361 KEFIIIFNREKLR-----QQGHGQSLDLDGRIGSQTSKLDQGR 400

RESULT 6
US-10-254-869-4
; Sequence 4, Application US/10254869
; Patent No. 6653117
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001160DIV
; CURRENT APPLICATION NUMBER: US/10/254,869
; CURRENT FILING DATE: 2002-09-26
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 404
; TYPE: PRT
; ORGANISM: Mus Musculus
US-10-254-869-4

Query Match 66.5%; Score 1430.5; DB 4; Length 404;
Best Local Similarity 68.1%; Pred. No. 1.6e-128;
Matches 280; Conservative 43; Mismatches 71; Indels 17; Gaps 5;
QY 1 MGANTSRRKPPVFDENEDVNFDPHFILRAIGKSGFGKVCIVQKNDTKKMYAMKYNKQCV 60
DB 1 MGNHSHKPPVFDENEVNFDFHQLRAIGKSGFGKVCIVQKNDTKKMYAMKYNKQCV 60
QY 61 -ERNEVRNVFKELQIMOGLEHPFLVNLWYSFQDEEDFMVVDLLGGDLRYHLQONVHFK 119
DB 61 QERDEVNRFRELQIMOGLEHPFLVNLWYSFQDEEDFMVVDLLGGDLRYHLQONVHFT 120
QY 120 EETVKLFICELVMDLYLQNRHIDMKPDNILLDEGHVHITDFNIAAMLPRETOITTT 179
DB 121 EGTVKLYICELALALEYLQRYHIIHRDIPDNILLDEGHVHITDFNIAATVLSKSEKASS 180
QY 180 MAGTKPYMAPFSSRKAGYSFAVDWMSLGTAYELLGRPRPYHRSSTSSKEIVHT 237
DB 181 MAGTKPYMAPFSSRKAGYSFAVDWMSLGTAYELLGRPRPYHRSATPIDEILNM 240
QY 238 FETTVVTPSAWSQEWVSLKLLKLEPNPDQRFQSDVQNFPMYNDINWDAVFKRLIPG 297
DB 241 FKVERVHYSTWCEGMVSLKLLKLTQDPESRLSLRDIQSWTYLADNWDNDAVFEKALMPG 300
QY 298 FPNKGRNLCDPTFELEEMILESKPLHKKKRLAK-KEKDMRKCDSSOTCLLOHLSVQ 356
DB 301 FPNKGRNLCDPTFELEEMILESKPLHKKKRLAKHRSRSTKDCSPLNGHLOQCLETVR 360
QY 357 KEFIIIFNREKVNRFNKRQPNLALQTKDPQVT--NQMDTGLSETFQTSK 405
DB 361 KEFIIIFNREKLR-----QQGHGQSLDLDGRIGSQTSKLDQGR 400

RESULT 7
US-09-801-876B-5
; Sequence 5, Application US/09801876B
; Patent No. 6492155
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001160

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; CURRENT APPLICATION NUMBER: US/09/801.876B
; CURRENT FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Human
US-09-801-876B-5

Query Match      66.2%; Score 1423.5; DB 4; Length 403;
Best Local Similarity 72.3%; Pred. No. 7.4e-128;
Matches 269; Conservative 40; Mismatches 60; Indels 3; Gaps 2;

Qy      1  MGNTSRKPPVFDEDEDVNFDFEILRAIGKSGFGKVCIVQKNDTKMYAMKYNKQKCV 60
Db      1  MGNHSHKPPVFDEDEDVNFDFEILRAIGKSGFGKVCIVQKNDTKMYAMKYNKQKCI 60

Qy      61  ERNEVRNVFKELQIMQGLEHFLVNLWYSFQDEEDFMVVDLLGGDLRYHLQONVHFKE 120
Db      61  ERDEVRNVFRELQIMQGLEHFLVNLWYSFQDEEDFMVVDLLGGDLRYHLQONVHFT 120

Qy      121  ETVKLFICELVMDALYQNRQRIHRDKMKNLILDEHGHVHITDFNTAAMLPRTOITTM 180
Db      121  GTVKLYICELALALEYLQRYHIHRDIKPDNILLDEHGHVHITDFNATVVGGAERASSM 180

Qy      181  AGTKPYMAPEMFS--SRKAGYSFAVDWWSLGVTAPELLRGRPPYHRSSTSSKEIVHTF 238
Db      181  AGTKPYMAPEVQVYMDRPGYSFVDWWSLGVTAPELLRGRPPYHRSVTPIDEILNMF 240

Qy      239  ETTVVTPYSAWSQEMVSLKLLPEPNDQRFQSDVQNFYPMNDINWDVAFQKRLIPGF 298
Db      239  ETTVVTPYSAWSQEMVSLKLLPEPNDQRFQSDVQNFYPMNDINWDVAFQKRLIPGF 298

Qy      241  KVERVHYSSTWCKGMVALLRKLTKDPESVSSLHDIQSVPYLADMNDVAFVKALMPGF 300
Db      241  KVERVHYSSTWCKGMVALLRKLTKDPESVSSLHDIQSVPYLADMNDVAFVKALMPGF 300

Qy      299  IPNKGRLNCDPTFELEEMILESPLHKKKRLAK-KEKDMRKCDSSTCLLQEHLDVQK 357
Db      299  IPNKGRLNCDPTFELEEMILESPLHKKKRLAK-KEKDMRKCDSSTCLLQEHLDVQK 357

Qy      301  VPNGRLNCDPTFELEEMILESPLHKKKRLAK-KEKDMRKCDSSTCLLQEHLDVQK 360
Db      301  VPNGRLNCDPTFELEEMILESPLHKKKRLAK-KEKDMRKCDSSTCLLQEHLDVQK 360

Qy      358  EFIFNREKVR 369
Db      361  EFIFNREKLRR 372

RESULT 8
US-10-254-869-5
; Sequence 5, Application US/10254869
; Patent No. 6653117
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001160DIV
; CURRENT APPLICATION NUMBER: US/10/254.869
; CURRENT FILING DATE: 2002-09-26
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Human
US-10-254-869-5

Query Match      66.2%; Score 1423.5; DB 4; Length 403;
Best Local Similarity 72.3%; Pred. No. 7.4e-128;
Matches 269; Conservative 40; Mismatches 60; Indels 3; Gaps 2;

Qy      1  MGNTSRKPPVFDEDEDVNFDFEILRAIGKSGFGKVCIVQKNDTKMYAMKYNKQKCV 60
Db      1  MGNHSHKPPVFDEDEDVNFDFEILRAIGKSGFGKVCIVQKNDTKMYAMKYNKQKCI 60

Qy      61  ERNEVRNVFKELQIMQGLEHFLVNLWYSFQDEEDFMVVDLLGGDLRYHLQONVHFKE 120
Db      61  ERDEVRNVFRELQIMQGLEHFLVNLWYSFQDEEDFMVVDLLGGDLRYHLQONVHFT 120

Qy      121  ETVKLFICELVMDALYQNRQRIHRDKMKNLILDEHGHVHITDFNTAAMLPRTOITTM 180
Db      121  GTVKLYICELALALEYLQRYHIHRDIKPDNILLDEHGHVHITDFNATVVGGAERASSM 180

Qy      181  AGTKPYMAPEMFS--SRKAGYSFAVDWWSLGVTAPELLRGRPPYHRSSTSSKEIVHTF 238
Db      181  AGTKPYMAPEVQVYMDRPGYSFVDWWSLGVTAPELLRGRPPYHRSVTPIDEILNMF 240

Qy      239  ETTVVTPYSAWSQEMVSLKLLPEPNDQRFQSDVQNFYPMNDINWDVAFQKRLIPGF 298
Db      239  ETTVVTPYSAWSQEMVSLKLLPEPNDQRFQSDVQNFYPMNDINWDVAFQKRLIPGF 298

Qy      241  KVERVHYSSTWCKGMVALLRKLTKDPESVSSLHDIQSVPYLADMNDVAFVKALMPGF 300
Db      241  KVERVHYSSTWCKGMVALLRKLTKDPESVSSLHDIQSVPYLADMNDVAFVKALMPGF 300

Qy      299  IPNKGRLNCDPTFELEEMILESPLHKKKRLAK-KEKDMRKCDSSTCLLQEHLDVQK 357
Db      299  IPNKGRLNCDPTFELEEMILESPLHKKKRLAK-KEKDMRKCDSSTCLLQEHLDVQK 357

Qy      301  VPNGRLNCDPTFELEEMILESPLHKKKRLAK-KEKDMRKCDSSTCLLQEHLDVQK 360
Db      301  VPNGRLNCDPTFELEEMILESPLHKKKRLAK-KEKDMRKCDSSTCLLQEHLDVQK 360

Qy      358  EFIFNREKVR 369
Db      361  EFIFNREKLRR 372

RESULT 9
US-09-799-875-14
; Sequence 14, Application US/09799875
; Patent No. 6638721
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Williamson, Mark
; TITLE OF INVENTION: No. 6638721el Human Protein Kinases and Uses
; TITLE OF INVENTION: Therefor
; FILE REFERENCE: 35800/209996
; CURRENT APPLICATION NUMBER: US/09/799.875
; CURRENT FILING DATE: 2001-03-06
; PRIOR FILING DATE: 2000-02-11
; PRIOR FILING DATE: 2000-02-11
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-799-875-14

Query Match      61.9%; Score 1332.5; DB 4; Length 419;
Best Local Similarity 65.0%; Pred. No. 4e-119;
Matches 253; Conservative 55; Mismatches 76; Indels 5; Gaps 3;

Qy      1  MGNTSRKPPVFDEDEDVNFDFEILRAIGKSGFGKVCIVQKNDTKMYAMKYNKQKCV 60
Db      5  MSAATARR-PVFDDKEDVNFDFEILRAIGKSGFGKVCIVQKNDTKMYAMKYNKQKCI 63

Qy      61  ERNEVRNVFKELQIMQGLEHFLVNLWYSFQDEEDFMVVDLLGGDLRYHLQONVHFKE 120
Db      64  ERDEVRNVFRELQIMQGLEHFLVNLWYSFQDEEDFMVVDLLGGDLRYHLQONVQFSE 123

Qy      121  ETVKLFICELVMDALYQNRQRIHRDKMKNLILDEHGHVHITDFNTAAMLPRTOITTM 180
Db      124  DTVRLVYICEMALDYLGRQHIHRDVKPDNILLDERGHAHLTDFNTATIKDGERATAL 183

Qy      181  AGTKPYMAPEMFS--RKGAGYSFAVDWWSLGVTAPELLRGRPPYHRSSTSSKEIVHTF 238
Db      184  AGTKPYMAPEIFHSFVNGGTGYSFVDWWSLGVTAPELLRGRPPYHRSNAVESLQOLF 243

Qy      239  ETTVVTPYSAWSQEMVSLKLLPEPNDQRFQSDVQNFYPMNDINWDVAFQKRLIPGF 298
Db      244  STVSQVQVPTWSKEMVALLRKLTKDPESVSSLHDIQSVPYLADMNDVAFVKALMPGF 303

Qy      299  IPNKGRLNCDPTFELEEMILESPLHKKKRLAK-KEKDMRKCDSSTCLLQEHLDVQK 356
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Db 304 VPKGRHLCHDFTFELEEMILESPLHKKKRLAKNKSQSDNSQSENQSDYLCCLDAIQ 363
Qy 357 KEFIFNREKYNRDNFKRQPNLALEQTKD 385
Db 364 QDFVIFNREKLRQDLPREPLPAPESRD 392

RESULT 10

US-09-801-876B-6
; Sequence 6, Application US/09801876B
; Patent No. 6492155
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001160
; CURRENT APPLICATION NUMBER: US/09/801,876B
; CURRENT FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Mus Musculus
US-09-801-876B-6

Query Match 61.8%; Score 1328.5; DB 4; Length 384;
Best Local Similarity 64.5%; Pred. No. 8.6e-119;
Matches 251; Conservative 55; Mismatches 74; Indels 9; Gaps 3;
Qy 6 SRKPPVFDENEDVNFDPHFILRAIGKSGFGKVCIVQKNDTKMYAMKYNKQKVERNEV 65
Db 1 SARPPVDDKEDVNFDPHFILRAIGKSGFGKVCIVQKRDTEKMYAMKYNKQCIERDEV 60
Qy 66 RNVPKELQIMQGLEHPEFLVNLWYSFQDEDMFMVVDLLGGDLRYHLQONVHFKEETVKL 125
Db 61 RNVPRELEILQIEHPEFLVNLWYSFQDEDMFMVVDLLGGDLRYHLQONVQFSEDTVRL 120
Qy 126 FICELVMDLYLQNRRIHRDMKPDNILLDEHGHVHTDFNIAAMLPRETOITTMAGTKP 185
Db 121 YICEMALDYLRSQHIIHRDVKPDNILLDQGHHLTDFNIATIIKDGERTALAGTKP 180
Qy 186 YMAPEMFSS--RKGAGYSFVDMWSLGVTAVELLRGRPPYHRSSTSKSKEIVHFTETVV 243
Db 181 YMAPEIFHSFVNGGTGYSEFVDMWSGVMAVELLRGRPPYDIHSSNAVESLVQLFSTVS 240
Qy 244 TYPSSAWSEMVSLLKLEPNPDQFSQSDVQNFPMYNDINMDAVFQKRLIPGFIPIKNG 303
Db 241 QYVPTWSKEMVALLKLLTVNPEHRFSSLDQMOTAPSLAHVLWDDLSEKKVPEPGFVPNG 300
Qy 304 RLNCDDPTFELEEMILESPLHKKKRLAKKEKMRKCDSSQT--CLLOEHLDSVQKEFII 361
Db 301 RLHCDDPTFELEEMILESPLHKKKRLAKNKSRRSSQSENQSDYLCCLDAIQDFVI 360
Qy 362 FNREKVRNDFNKRQPNLALEQTKDPQVTN 390
Db 361 FNREKL-----KRSQELMSEPPPGPETS 384

RESULT 11

US-10-254-869-6
; Sequence 6, Application US/10254869
; Patent No. 6653117
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001160DIV
; CURRENT APPLICATION NUMBER: US/10/254,869
; CURRENT FILING DATE: 2002-09-26

; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Mus Musculus
US-10-254-869-6

Query Match 61.8%; Score 1328.5; DB 4; Length 384;
Best Local Similarity 64.5%; Pred. No. 8.6e-119;
Matches 251; Conservative 55; Mismatches 74; Indels 9; Gaps 3;
Qy 6 SRKPPVFDENEDVNFDPHFILRAIGKSGFGKVCIVQKNDTKMYAMKYNKQKVERNEV 65
Db 1 SARPPVDDKEDVNFDPHFILRAIGKSGFGKVCIVQKRDTEKMYAMKYNKQCIERDEV 60
Qy 66 RNVPKELQIMQGLEHPEFLVNLWYSFQDEDMFMVVDLLGGDLRYHLQONVHFKEETVKL 125
Db 61 RNVPRELEILQIEHPEFLVNLWYSFQDEDMFMVVDLLGGDLRYHLQONVQFSEDTVRL 120
Qy 126 FICELVMDLYLQNRRIHRDMKPDNILLDEHGHVHTDFNIAAMLPRETOITTMAGTKP 185
Db 121 YICEMALDYLRSQHIIHRDVKPDNILLDQGHHLTDFNIATIIKDGERTALAGTKP 180
Qy 186 YMAPEMFSS--RKGAGYSFVDMWSLGVTAVELLRGRPPYHRSSTSKSKEIVHFTETVV 243
Db 181 YMAPEIFHSFVNGGTGYSEFVDMWSGVMAVELLRGRPPYDIHSSNAVESLVQLFSTVS 240
Qy 244 TYPSSAWSEMVSLLKLEPNPDQFSQSDVQNFPMYNDINMDAVFQKRLIPGFIPIKNG 303
Db 241 QYVPTWSKEMVALLKLLTVNPEHRFSSLDQMOTAPSLAHVLWDDLSEKKVPEPGFVPNG 300
Qy 304 RLNCDDPTFELEEMILESPLHKKKRLAKKEKMRKCDSSQT--CLLOEHLDSVQKEFII 361
Db 301 RLHCDDPTFELEEMILESPLHKKKRLAKNKSRRSSQSENQSDYLCCLDAIQDFVI 360
Qy 362 FNREKVRNDFNKRQPNLALEQTKDPQVTN 390
Db 361 FNREKL-----KRSQELMSEPPPGPETS 384

RESULT 12
US-09-819-607-4
; Sequence 4, Application US/09819607
; Patent No. 6686176
; GENERAL INFORMATION:
; APPLICANT: BEASLEY, Ellen et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001078
; CURRENT APPLICATION NUMBER: US/09/819,607
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-819-607-4

Query Match 60.2%; Score 1294.5; DB 4; Length 399;
Best Local Similarity 63.4%; Pred. No. 1.6e-115;
Matches 248; Conservative 54; Mismatches 80; Indels 9; Gaps 3;
Qy 18 VNFDFEILRAIGKSGFGKVCIVQKNDTKMYAMKYNKQKVERNEVNFKEIQIMQG 77
Db 1 VNFDFEILRAIGKSGFGKVCIVQKRDTEKMYAMKYNKQCIERDEVNFRELEIQE 60
Qy 78 LEHPEFLVNLWYSFQDEDMFMVVDLLGGDLRYHLQONVHFKEETVKLFCELVMDLYL 137
Db 61 LEHPEFLVNLWYSFQDEDMFMVVDLLGGDLRYHLQONVQFSEDTVRLVICEMALDYL 120

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QY 138 QNQRHHRMCKPDNILLDEHGHVHTDFNIAAMLPRETQITTMAGCTKPYMAPEMPSS--R 195
Db 121 RSQHIIHRDVKPDNILLDEHGHVHTDFNIAAMLPRETQITTMAGCTKPYMAPEMPSS--R 180
QY 196 KGAGYSEAVDWSLGVAYELLGRPRPHIRSSSTSSKEIVHTFETVTVTPSANSOEMVS 255
Db 181 GGTGYSFEVDWWSGVAYELLGRPRPHIRSSSTSSKEIVHTFETVTVTPSANSOEMVS 240
QY 256 LKLLLEPNPDRFQSLQDVQNFYPMNDINMDAVFQKRLIPGIPNKGRLNCDPTFFEE 315
Db 241 LLKLLTVNPEHFFSLQDMQAPSLAHVMDLSEKKVEGFPVFNKGRLLHCDPTFFEE 300
QY 316 MILESPLHKKKRLAKKEMKRCDSST--CLLQEHLDVQKBFIFNREKVNDRPNK 373
Db 301 MILESPLHKKKRLAKKEMKRCDSST--CLLQEHLDVQKBFIFNREKVNDRPNK 360
QY 374 RQNLALQTKDPQVNTGMDTGLSETQTS 404
Db 386 RQELMSEPPPGFETSDMTDSTADSEAPTA 386
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RESULT 13
US-09-841-683-7
; Sequence 7, Application US/09841683
; Patent No. 6617147
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Nepomnichy, Boris
; APPLICANT: Wang, Xiaoming
; APPLICANT: Donoho, Gregory
; APPLICANT: Scoville, John
; APPLICANT: Walke, D. Wade
; TITLE OF INVENTION: No. 6617147el Human Kinase Proteins and Polynucleotides Encoding
; FILE REFERENCE: LEX-0167-USA
; CURRENT APPLICATION NUMBER: US/09/841,683
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: US 60/199,499
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US 60/201,227
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 236
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-841-683-7
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Query Match 54.6%; Score 1174; DB 4; Length 236;
Best Local Similarity 91.1%; Pred. No. 2.7e-104;
Matches 224; Conservative 1; Mismatches 1; Indels 20; Gaps 1;

QY 1 MGATSRKPPVFDENEDVNFDFEILRAIGKSGFKVCIVQKNDTKMYAMKYNKQKV 60
Db 1 MGATSRKPPVFDENEDVNFDFEILRAIGKSGFKVCIVQKNDTKMYAMKYNKQKV 60
QY 61 ERNEVRNVFKELIQMOGLEHPPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQNVHPKE 120
Db 61 ERNEVRNVFKELIQMOGLEHPPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQNVHPKE 120
QY 121 ETVKLFICELVMDLYLQNRHHRMCKPDNILLDEHGHVHTDFNIAAMLPRETQITTM 180
Db 121 ETVKLFICELVMDLYLQNRHHRMCKPDNILLDEHGHVHTDFNIAAMLPRETQITTM 180
QY 181 AGTKPYMAPEMPSSRKAGYSFAVDWWSLGVAYELLGRPRPHIRSSSTSSKEIVHTFET 240
Db 181 AGTKPYMAPEMPSSRKAGYSFAVDWWSLGVAYELLGRPRPHIRSSSTSSKEIVHTFET 240
QY 241 TVVTVTP 246
Db 221 TVVAEP 226
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RESULT 14
US-09-841-683-5
; Sequence 5, Application US/09841683
; Patent No. 6617147
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Nepomnichy, Boris
; APPLICANT: Wang, Xiaoming
; APPLICANT: Donoho, Gregory
; APPLICANT: Scoville, John
; APPLICANT: Walke, D. Wade
; TITLE OF INVENTION: No. 6617147el Human Kinase Proteins and Polynucleotides Encoding
; FILE REFERENCE: LEX-0167-USA
; CURRENT APPLICATION NUMBER: US/09/841,683
; CURRENT FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: US 60/199,499
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US 60/201,227
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 225
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-841-683-5
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Best Local Similarity 100.0%; Pred. No. 4.8e-104;
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QY 1 MGATSRKPPVFDENEDVNFDFEILRAIGKSGFKVCIVQKNDTKMYAMKYNKQKV 60
Db 1 MGATSRKPPVFDENEDVNFDFEILRAIGKSGFKVCIVQKNDTKMYAMKYNKQKV 60
QY 61 ERNEVRNVFKELIQMOGLEHPPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQNVHPKE 120
Db 61 ERNEVRNVFKELIQMOGLEHPPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQNVHPKE 120
QY 121 ETVKLFICELVMDLYLQNRHHRMCKPDNILLDEHGHVHTDFNIAAMLPRETQITTM 180
Db 121 ETVKLFICELVMDLYLQNRHHRMCKPDNILLDEHGHVHTDFNIAAMLPRETQITTM 180
QY 181 AGTKPYMAPEMPSSRKAGYSFAVDWWSLGVAYELLGR 220
Db 181 AGTKPYMAPEMPSSRKAGYSFAVDWWSLGVAYELLGR 220
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RESULT 15
US-09-819-607-2
; Sequence 2, Application US/09819607
; Patent No. 6686176
; GENERAL INFORMATION:
; APPLICANT: BEASLEY, Ellen et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL001078
; CURRENT APPLICATION NUMBER: US/09/819,607
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Human
US-09-819-607-2
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Query Match 53.1%; Score 1142; DB 4; Length 369;
Best Local Similarity 63.2%; Pred. No. 5.8e-101;
Matches 216; Conservative 50; Mismatches 72; Indels 4; Gaps 2;

QY 48 MYAMKYNKQKVVERNEVRNVFKELIQMOGLEHPPFLVNLWYSFQDEEDMFVVDLLGGD 107
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Db      1 MYANKYKQOCIERDEVNFRLEBILQIEHVFNLWYSFQDEBDMFVVDLLGGD 60
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Db      61 LRYHLQONVQFSEDTVALYICEMALADYLRGQHIHRDVKPDNILLDERGHAHLTDFNI 120
Qy     168 AAMLPRETOITTMAGTKPYMAPENFSS--RKGAGYSFAVDWWSLGVTAAYELLRGRRPYHI 225
Db     121 ATIIKDGERTALAGTRPYMAPEIFHSFVNGGTGYSFEVDWWSGVMAAYELLRGWRPYDI 180
Qy     226 RSSTSKEIVHTFETTVVTPSAWSQEMVSLKLLLEPNPDORFSQLSDVQNPFPYMDIN 285
Db     181 HSSNAVSLSVLQFSTVSQYVPTWSKEMVALLRKLTTVNEHRLSSLODVOAAPALAGVL 240
Qy     286 WDAVFQKRLIPGFI PNKGRNLCDPTFELEEMILES KPLHKKKKLAKKEKDMRKCDSSQT 345
Db     241 WDHLSEKRVFPGFVFNKGRNLHCDPTFELEEMILES RPLHKKKKLAKNKRSDNSRDSQS 300
Qy     346 --CLLQEHLSVQKEFIIFNREKVNRPDKPNALAEQTKD 385
Db     301 ENDYLODCLDAIQODFVFNREKLKRSQDLPREPLPAPESRD 342

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Job time : 23 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 17, 2004, 09:28:08 ; Search time 946 Seconds
(without alignments)
153.952 Million cell updates/sec

Title: US-10-620-845-9

Perfect score: 2151

Sequence: 1 MGANTSRRPVPFEDNEDVNF.....VTNGQMDTGLSETFQTSKVS 407

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1589859 seqs, 357834939 residues

Total number of hits satisfying chosen parameters: 1589859

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pcp.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pcp.*
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- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pcp.*
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- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pcp.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pcp.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pcp.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pcp.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pcp.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pcp.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pcp.*
- 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pcp.*
- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pcp.*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2151	100.0	407	9	US-09-841-683-9
2	2151	100.0	407	16	US-10-620-845-9
3	2060	95.8	396	9	US-09-841-683-11
4	2060	95.8	396	14	US-10-288-798-20
5	2060	95.8	396	15	US-10-362-892-20
6	2060	95.8	396	15	US-10-182-243-33
7	2060	95.8	396	15	US-10-620-845-11
8	2054	95.5	396	15	US-10-410-764-101
9	2047	95.2	396	9	US-09-801-8768-2
10	2047	95.2	396	14	US-10-254-869-2
11	2047	95.2	396	15	US-10-667-442-2
12	1827	84.9	358	15	US-10-108-260A-2674
13	1441	67.0	414	15	US-10-074-978A-158

14	1430.5	66.5	404	9	US-09-801-8768-4	Sequence 4, Appli
15	1430.5	66.5	404	14	US-10-254-869-4	Sequence 4, Appli
16	1430.5	66.5	404	15	US-10-667-442-4	Sequence 4, Appli
17	1423.5	66.2	403	9	US-09-801-8768-5	Sequence 5, Appli
18	1423.5	66.2	403	14	US-10-254-869-5	Sequence 5, Appli
19	1423.5	66.2	403	15	US-10-667-442-5	Sequence 5, Appli
20	1423.5	66.2	414	14	US-10-354-358-36	Sequence 36, Appli
21	1423.5	66.2	414	15	US-10-074-978A-157	Sequence 157, App
22	1423.5	62.0	488	15	US-10-074-978A-154	Sequence 154, App
23	1332.5	61.9	419	9	US-09-799-875-14	Sequence 14, Appli
24	1332.5	61.9	419	14	US-10-303-664A-6	Sequence 6, Appli
25	1332.5	61.9	419	15	US-10-649-156-14	Sequence 14, Appli
26	1332.5	61.9	485	17	US-10-618-941-75	Sequence 75, Appli
27	1331	61.9	485	15	US-10-415-011-12	Sequence 12, Appli
28	1328.5	61.8	384	9	US-09-801-8768-6	Sequence 6, Appli
29	1328.5	61.8	384	14	US-10-254-869-6	Sequence 6, Appli
30	1328.5	61.8	384	15	US-10-667-442-6	Sequence 18, Appli
31	1310.5	60.9	488	15	US-10-074-978A-18	Sequence 4, Appli
32	1294.5	60.2	399	10	US-09-819-607-4	Sequence 4, Appli
33	1294.5	60.2	399	15	US-10-633-631-4	Sequence 4, Appli
34	1272.5	59.2	375	15	US-10-168-582-12	Sequence 12, Appli
35	1186.5	55.2	364	13	US-10-052-586-572	Sequence 572, App
36	1186.5	55.2	364	14	US-10-174-590-572	Sequence 572, App
37	1186.5	55.2	364	14	US-10-176-758-572	Sequence 572, App
38	1186.5	55.2	364	14	US-10-175-737-572	Sequence 572, App
39	1186.5	55.2	364	14	US-10-174-581-572	Sequence 572, App
40	1186.5	55.2	364	14	US-10-176-483-572	Sequence 572, App
41	1186.5	55.2	364	14	US-10-176-749-572	Sequence 572, App
42	1186.5	55.2	364	14	US-10-176-914-572	Sequence 572, App
43	1186.5	55.2	364	14	US-10-176-915-572	Sequence 572, App
44	1186.5	55.2	364	14	US-10-173-706-572	Sequence 572, App
45	1186.5	55.2	364	14	US-10-175-738-572	Sequence 572, App

ALIGNMENTS

RESULT 1

US-09-841-683-9
; Sequence 9, Application US/09841683
; Patent No. US20020081600A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Nepomnichy, Boris
; APPLICANT: Wang, Xiaoming
; APPLICANT: Donoho, Gregory
; APPLICANT: Scoville, John
; APPLICANT: Walke, D. Wade
; TITLE OF INVENTION: No. US20020081600A1 Human Kinase Proteins and Polynucleotides
; FILE REFERENCE: LEX-0167-USA
; CURRENT APPLICATION NUMBER: US/09/841,683
; CURRENT FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: US 60/199,499
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US 60/201,227
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 407
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-841-683-9

Query Match 100.0%; Score 2151; DB 9; Length 407;

Best Local Similarity 100.0%; Pred. No. 7.2e-153;

Matches 407; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGANTSRRPVPFEDNEDVNFHFEILRAIGKSGFKVICIVQKNDTKQYAMKYNKQKCV 60

Db 1 MGANTSRRPVPFEDNEDVNFHFEILRAIGKSGFKVICIVQKNDTKQYAMKYNKQKCV 60

Qy 61 ERNEVRNVFKELQIMQGLEHPPFLVNLVYSQDEEDFMVVDLLGGDLRYHLQNVHFK 120

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Db      61  ERNEVRNVFKELQIMQGLEHPEFLVNLWYSFQDEEDMFVVDLLGGDLRHLQONVHFKE 120
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Db      121  ETVKLFICELVWALDYLNQRIIHRDMKPDNILLDEGHVHITDFNIAAMLPRETOITTM 180
Qy      181  AGTKPYMAPENFSSRGKAGYSFAVDWWSLGTAYELLGRPPYHRSSTSSKEIVHTFET 240
Db      181  AGTKPYMAPENFSSRGKAGYSFAVDWWSLGTAYELLGRPPYHRSSTSSKEIVHTFET 240
Qy      241  TVVTYPSAWSQEMVSLKLLKLEPNPDQFQSDVQNFPPYMNNDINWDAVFOKRLIPGIP 300
Db      241  TVVTYPSAWSQEMVSLKLLKLEPNPDQFQSDVQNFPPYMNNDINWDAVFOKRLIPGIP 300
Qy      301  NKGRLNCDPTFELEEMILESPLHKKKRLAKKEDMRKCDSSQTCLLQEHLDVQKEFI 360
Db      301  NKGRLNCDPTFELEEMILESPLHKKKRLAKKEDMRKCDSSQTCLLQEHLDVQKEFI 360
Qy      361  IFNREKVRNDRKQPNLALQTKDPQVTNGQMDTGLSETFQTSKVS 407
Db      361  IFNREKVRNDRKQPNLALQTKDPQVTNGQMDTGLSETFQTSKVS 407
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RESULT 2

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US-10-620-845-9
; Sequence 9, Application US/10620845
; Publication No. US20040115693A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Nepomnichy, Boris
; APPLICANT: Wang, Xiaoming
; APPLICANT: Donoho, Gregory
; APPLICANT: Scoville, John
; APPLICANT: Walke, D. Wade
; TITLE OF INVENTION: Novel Human Kinase Proteins and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0167-USA
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: US/10/620,845
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: US/09/841,683
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: US 60/199,499
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US 60/201,227
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 407
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-620-845-9
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Query Match      100.0%; Score 2151; DB 15; Length 407;
Best Local Similarity 100.0%; Pred. No. 7.2e-153;
Matches 407; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      61  ERNEVRNVFKELQIMQGLEHPEFLVNLWYSFQDEEDMFVVDLLGGDLRHLQONVHFKE 120
Qy      121  ETVKLFICELVWALDYLNQRIIHRDMKPDNILLDEGHVHITDFNIAAMLPRETOITTM 180
Db      121  ETVKLFICELVWALDYLNQRIIHRDMKPDNILLDEGHVHITDFNIAAMLPRETOITTM 180
Qy      181  AGTKPYMAPENFSSRGKAGYSFAVDWWSLGTAYELLGRPPYHRSSTSSKEIVHTFET 240
Db      181  AGTKPYMAPENFSSRGKAGYSFAVDWWSLGTAYELLGRPPYHRSSTSSKEIVHTFET 240
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Qy      301  NKGRLNCDPTFELEEMILESPLHKKKRLAKKEDMRKCDSSQTCLLQEHLDVQKEFI 360
Db      301  NKGRLNCDPTFELEEMILESPLHKKKRLAKKEDMRKCDSSQTCLLQEHLDVQKEFI 360
Qy      361  IFNREKVRNDRKQPNLALQTKDPQVTNGQMDTGLSETFQTSKVS 407
Db      361  IFNREKVRNDRKQPNLALQTKDPQVTNGQMDTGLSETFQTSKVS 407

RESULT 3
US-09-841-683-11
; Sequence 11, Application US/09841683
; Patent No. US20020081600A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Nepomnichy, Boris
; APPLICANT: Wang, Xiaoming
; APPLICANT: Donoho, Gregory
; APPLICANT: Scoville, John
; APPLICANT: Walke, D. Wade
; TITLE OF INVENTION: No. US20020081600A1el Human Kinase Proteins and Polynucleotides E
; FILE REFERENCE: LEX-0167-USA
; CURRENT FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: US 60/199,499
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US 60/201,227
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 396
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-841-683-11

Query Match      95.8%; Score 2060; DB 9; Length 396;
Best Local Similarity 99.2%; Pred. No. 4.6e-146;
Matches 389; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Db      1  MGANTSRRKPPVDENEDVNFDFEILRAIGKSGFGKVCIVQKNDTKOMYAMKYNKQKCV 60
Qy      61  ERNEVRNVFKELQIMQGLEHPEFLVNLWYSFQDEEDMFVVDLLGGDLRHLQONVHFKE 120
Db      61  ERNEVRNVFKELQIMQGLEHPEFLVNLWYSFQDEEDMFVVDLLGGDLRHLQONVHFKE 120
Qy      121  ETVKLFICELVWALDYLNQRIIHRDMKPDNILLDEGHVHITDFNIAAMLPRETOITTM 180
Db      121  ETVKLFICELVWALDYLNQRIIHRDMKPDNILLDEGHVHITDFNIAAMLPRETOITTM 180
Qy      181  AGTKPYMAPENFSSRGKAGYSFAVDWWSLGTAYELLGRPPYHRSSTSSKEIVHTFET 240
Db      181  AGTKPYMAPENFSSRGKAGYSFAVDWWSLGTAYELLGRPPYHRSSTSSKEIVHTFET 240
Qy      241  TVVTYPSAWSQEMVSLKLLKLEPNPDQFQSDVQNFPPYMNNDINWDAVFOKRLIPGIP 300
Db      241  TVVTYPSAWSQEMVSLKLLKLEPNPDQFQSDVQNFPPYMNNDINWDAVFOKRLIPGIP 300
Qy      301  NKGRLNCDPTFELEEMILESPLHKKKRLAKKEDMRKCDSSQTCLLQEHLDVQKEFI 360
Db      301  NKGRLNCDPTFELEEMILESPLHKKKRLAKKEDMRKCDSSQTCLLQEHLDVQKEFI 360
Qy      361  IFNREKVRNDRKQPNLALQTKDPQVTNGQMDTGLSETFQTSKVS 392
Db      361  IFNREKVRNDRKQPNLALQTKDPQVTNGQMDTGLSETFQTSKVS 392
```

```
RESULT 4
US-10-288-798-20
; Sequence 20, Application US/10288798
; Publication No. US20030207299A1
; GENERAL INFORMATION:
; APPLICANT: BANDMAN, Olga; NGUYEN, Daniel B.; HAFALIA, April J.A.;
; APPLICANT: WALIA, Narinder K.; HAFALIA, April J.A.;
; APPLICANT: YAO, Monique G.; GANDHI, Ameena R.;
; APPLICANT: GURURAJAN, Rajagopal; DING, Li;
; APPLICANT: PATTERSON, Chandra; YUE, Henry;
; APPLICANT: BAUGHN, Mariah R.; TRIBOULEY, Catherine M.;
; APPLICANT: THORNTON, Michael; ELLIOTT, Vicki S.;
; APPLICANT: LU, Yan; ISON, Craig H.;
; APPLICANT: AU-YOUNG, Janice; TANG, Y. Tom;
; APPLICANT: AZIMZAI, Yalda; BURRILL, John D.;
; APPLICANT: MARCUS, Gregory A.; ZINGLER, Kurt A.;
; APPLICANT: LU, Dyung Aina M.; LAL, Preeti G.;
; APPLICANT: RAMKUMAR, Javalaxmi; WARREN, Bridget A.;
; APPLICANT: KEARNEY, Liam; POLICKY, Jennifer L.;
; APPLICANT: THANGAVELU, Kavitha; BURFORD, Neil
; TITLE OF INVENTION: HUMAN KINASES
; FILE REFERENCE: PI-0209 USA
; CURRENT APPLICATION NUMBER: US/10/288,798
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: PCT/US01/27219
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/240,542
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: US 60/238,389
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 60/236,499
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: US 60/234,902
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US 60/232,654
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US 60/231,357
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: US 60/229,873
; PRIOR FILING DATE: 2000-08-31
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PERL Program
; SEQ ID NO 20
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030207299A1 794584CD1
US-10-288-798-20

Query Match 95.8%; Score 2060; DB 14; Length 396;
Best Local Similarity 99.2%; Pred. No. 4.6e-146;
Matches 389; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MGANTSRRKPPVFDENEDVDFHFEILRAIGKSGFGKVCIVQKNDTKQYAMKYNKQKCV 60
Db 1 MGANTSRRKPPVFDENEDVDFHFEILRAIGKSGFGKVCIVQKNDTKQYAMKYNKQKCV 60

Qy 61 ERNEVRNVFKELQIMQGLEHFFLVNLWYSQDEDMFVVDLLGGDLRYHLOQNVHFK 120
Db 61 ERNEVRNVFKELQIMQGLEHFFLVNLWYSQDEDMFVVDLLGGDLRYHLOQNVHFK 120

Qy 121 ETVKLFICELVMDLYLQNRITHRDKMPNILLDEHGHVHITDFNTAAMLPRETQITTM 180
Db 121 ETVKLFICELVMDLYLQNRITHRDKMPNILLDEHGHVHITDFNTAAMLPRETQITTM 180

Qy 181 AGTKPYMAPFSSRRKAGYSFAVDWWSLGVATYELLGRRPYHIRSTSSKEIVHTFET 240
Db 181 AGTKPYMAPFSSRRKAGYSFAVDWWSLGVATYELLGRRPYHIRSTSSKEIVHTFET 240

Qy 241 TVVTYPSANQSEMVSLKLLLEPNPQDFSQLSDVQNFPPYMNNDINWDAVQKRLIPGFI 300
Db 241 TVVTYPSANQSEMVSLKLLLEPNPQDFSQLSDVQNFPPYMNNDINWDAVQKRLIPGFI 300
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RESULT 5
US-10-362-892-20
; Sequence 20, Application US/10362892
; Publication No. US20040038881A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.; BANDMAN, Olga
; APPLICANT: NGUYEN, Daniel B.; WALIA, Narinder K.
; APPLICANT: HAFALIA, April J.A.; YAO, Monique G.
; APPLICANT: GANDHI, Ameena R.; GURURAJAN, Rajagopal
; APPLICANT: DING, Li; PATTERSON, Chandra S.
; APPLICANT: YUE, Henry; BAUGHN, Mariah R.
; APPLICANT: TRIBOULEY, Catherine M.; THORNTON, Michael B.
; APPLICANT: ELLIOTT, Vicki S.; LU, Yan
; APPLICANT: ISON, Craig H.; AU-YOUNG, Janice K.
; APPLICANT: TANG, Y. Tom; AZIMZAI, Yalda
; APPLICANT: BURRILL, John D.; MARCUS, Gregory A.
; APPLICANT: ZINGLER, Kurt A.; LU, Dyung Aina M.
; APPLICANT: LAL, Preeti G.; RAMKUMAR, Javalaxmi
; APPLICANT: WARREN, Bridget A.; KEARNEY, Liam
; APPLICANT: POLICKY, Jennifer L.; THANGAVELU, Kavitha
; APPLICANT: BURFORD, Neil
; TITLE OF INVENTION: HUMAN KINASES
; FILE REFERENCE: PF-0209 USN
; CURRENT APPLICATION NUMBER: US/10/362,892
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: PCT/US01/27219
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,873
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US 60/231,357
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: US 60/232,654
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US 60/234,902
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US 60/236,499
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: US 60/238,389
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 60/240,542
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PERL Program
; SEQ ID NO 20
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040038881A1 794584CD1
US-10-362-892-20

Query Match 95.8%; Score 2060; DB 15; Length 396;
Best Local Similarity 99.2%; Pred. No. 4.6e-146;
Matches 389; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MGANTSRRKPPVFDENEDVDFHFEILRAIGKSGFGKVCIVQKNDTKQYAMKYNKQKCV 60
Db 1 MGANTSRRKPPVFDENEDVDFHFEILRAIGKSGFGKVCIVQKNDTKQYAMKYNKQKCV 60

Qy 61 ERNEVRNVFKELQIMQGLEHFFLVNLWYSQDEDMFVVDLLGGDLRYHLOQNVHFK 120
Db 61 ERNEVRNVFKELQIMQGLEHFFLVNLWYSQDEDMFVVDLLGGDLRYHLOQNVHFK 120
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Db 61 ERNEVRNVFKELQIMQGLEHFFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKE 120
Qy 121 ETVKLFICELVWALDYLNQRIIHRDMKPDNILLDEHGHVHITDFNTAAMLPRETOITTM 180
Db 121 ETVKLFICELVWALDYLNQRIIHRDMKPDNILLDEHGHVHITDFNTAAMLPRETOITTM 180
Qy 181 AGTKPYMAPEMFSSRKAGYGFVADWWSLGTAVAYELLGRRPYHRSSTSSKEIVHTFET 240
Db 181 AGTKPYMAPEMFSSRKAGYGFVADWWSLGTAVAYELLGRRPYHRSSTSSKEIVHTFET 240
Qy 241 TVVTYPSAWSQEMVSLKLLLEPNPDQRFSDVQNFPPYMNNDINWDAVFKRLIPGIP 300
Db 241 TVVTYPSAWSQEMVSLKLLLEPNPDQRFSDVQNFPPYMNNDINWDAVFKRLIPGIP 300
Qy 301 NKGRINCDPTFELEMILESPLHKKKRLAKKEDMKRCDSSQTCLLQEHLDVQKEFI 360
Db 301 NKGRINCDPTFELEMILESPLHKKKRLAKKEDMKRCDSSQTCLLQEHLDVQKEFI 360
Qy 361 IFNREKVNDRDNFKQPNLALEQTKDPQVINGQ 392
Db 361 IFNREKVNDRDNFKQPNLALEQTKDPQGEDGQ 392

RESULT 6

US-10-182-243-33
; Sequence 33, Application US/10182243
; Publication No. US20040048310A1
; GENERAL INFORMATION:
; APPLICANT: FLOWMAN, GREGORY D.
; APPLICANT: WHITE, DAVID
; APPLICANT: MANNING, GERARD
; APPLICANT: SUDARSANAN, SUCHA
; APPLICANT: MARTINEZ, RICARDO
; TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES AND PROTEIN KINASE-LIKE
; TITLE OF INVENTION: ENZYMES
; FILE REFERENCE: 038602/1366
; CURRENT APPLICATION NUMBER: US/10/182,243
; CURRENT FILING DATE: 2003-07-07
; PRIOR APPLICATION NUMBER: PCT/US01/02337
; PRIOR FILING DATE: 2001-01-25
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 33
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-243-33

Query Match 95.8%; Score 2060; DB 15; Length 396;
Best Local Similarity 99.2%; Pred. No. 4.6e-146;
Matches 389; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 1 MGANTSRRKPPVFDENEDVNFDFEILRAIGKSGFGKVCIVQKNDTKQWAMKYNKQKCV 60
Db 1 MGANTSRRKPPVFDENEDVNFDFEILRAIGKSGFGKVCIVQKNDTKQWAMKYNKQKCV 60
Qy 61 ERNEVRNVFKELQIMQGLEHFFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKE 120
Db 61 ERNEVRNVFKELQIMQGLEHFFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKE 120
Qy 121 ETVKLFICELVWALDYLNQRIIHRDMKPDNILLDEHGHVHITDFNTAAMLPRETOITTM 180
Db 121 ETVKLFICELVWALDYLNQRIIHRDMKPDNILLDEHGHVHITDFNTAAMLPRETOITTM 180
Qy 181 AGTKPYMAPEMFSSRKAGYGFVADWWSLGTAVAYELLGRRPYHRSSTSSKEIVHTFET 240
Db 181 AGTKPYMAPEMFSSRKAGYGFVADWWSLGTAVAYELLGRRPYHRSSTSSKEIVHTFET 240
Qy 241 TVVTYPSAWSQEMVSLKLLLEPNPDQRFSDVQNFPPYMNNDINWDAVFKRLIPGIP 300
Db 241 TVVTYPSAWSQEMVSLKLLLEPNPDQRFSDVQNFPPYMNNDINWDAVFKRLIPGIP 300
Qy 301 NKGRINCDPTFELEMILESPLHKKKRLAKKEDMKRCDSSQTCLLQEHLDVQKEFI 360

Db 301 NKGRINCDPTFELEMILESPLHKKKRLAKKEDMKRCDSSQTCLLQEHLDVQKEFI 360
Qy 361 IFNREKVNDRDNFKQPNLALEQTKDPQVINGQ 392
Db 361 IFNREKVNDRDNFKQPNLALEQTKDPQGEDGQ 392
RESULT 7
US-10-620-845-11
; Sequence 11, Application US/10620845
; Publication No. US20040115693A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Nepomnichy, Boris
; APPLICANT: Wang, Xiaoming
; APPLICANT: Donoho, Gregory
; APPLICANT: Scoville, John
; APPLICANT: Walke, D. Wade
; TITLE OF INVENTION: Novel Human Kinase Proteins and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0167-USA
; CURRENT APPLICATION NUMBER: US/10/620,845
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: US/09/841,683
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: US 60/199,499
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US 60/201,227
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 396
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-620-845-11

Query Match 95.8%; Score 2060; DB 16; Length 396;
Best Local Similarity 99.2%; Pred. No. 4.6e-146;
Matches 389; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 1 MGANTSRRKPPVFDENEDVNFDFEILRAIGKSGFGKVCIVQKNDTKQWAMKYNKQKCV 60
Db 1 MGANTSRRKPPVFDENEDVNFDFEILRAIGKSGFGKVCIVQKNDTKQWAMKYNKQKCV 60
Qy 61 ERNEVRNVFKELQIMQGLEHFFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKE 120
Db 61 ERNEVRNVFKELQIMQGLEHFFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKE 120
Qy 121 ETVKLFICELVWALDYLNQRIIHRDMKPDNILLDEHGHVHITDFNTAAMLPRETOITTM 180
Db 121 ETVKLFICELVWALDYLNQRIIHRDMKPDNILLDEHGHVHITDFNTAAMLPRETOITTM 180
Qy 181 AGTKPYMAPEMFSSRKAGYGFVADWWSLGTAVAYELLGRRPYHRSSTSSKEIVHTFET 240
Db 181 AGTKPYMAPEMFSSRKAGYGFVADWWSLGTAVAYELLGRRPYHRSSTSSKEIVHTFET 240
Qy 241 TVVTYPSAWSQEMVSLKLLLEPNPDQRFSDVQNFPPYMNNDINWDAVFKRLIPGIP 300
Db 241 TVVTYPSAWSQEMVSLKLLLEPNPDQRFSDVQNFPPYMNNDINWDAVFKRLIPGIP 300
Qy 301 NKGRINCDPTFELEMILESPLHKKKRLAKKEDMKRCDSSQTCLLQEHLDVQKEFI 360
Db 301 NKGRINCDPTFELEMILESPLHKKKRLAKKEDMKRCDSSQTCLLQEHLDVQKEFI 360
Qy 361 IFNREKVNDRDNFKQPNLALEQTKDPQVINGQ 392
Db 361 IFNREKVNDRDNFKQPNLALEQTKDPQGEDGQ 392

RESULT 8

US-10-410-764-101
; Sequence 101, Application US/10410764


```
Publication No. US20040005664A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Meyers, Rachel E.
APPLICANT: MacBeth, Kyle J.
APPLICANT: Curtis, Rory A.J.
APPLICANT: Rudolph-Owen, Laura A.
APPLICANT: Weich, Nadine S.
APPLICANT: Olandt, Peter J.
APPLICANT: Tsai, Fong-Ying
APPLICANT: Kapeller-Libermann, Rosana
APPLICANT: Carroll, Joseph M.
TITLE OF INVENTION: 26199, 33530, 33949, 47148, 50226,
58764, 62113, 32144, 32235, 23565, 13305, 14911, 86216,
25206 AND 8843 MOLECULES AND USES THEREFOR
TITLE OF INVENTION: 25206 AND 8843 MOLECULES AND USES THEREFOR
FILE REFERENCE: MPI03-05ZOMNIM
CURRENT APPLICATION NUMBER: US/10/410,764
CURRENT FILING DATE: 2003-04-10
PRIORITY APPLICATION NUMBER: US 09/924,358
PRIORITY FILING DATE: 2001-08-06
PRIORITY APPLICATION NUMBER: US 60/229,300
PRIORITY FILING DATE: 2000-09-01
PRIORITY APPLICATION NUMBER: US 10/350,553
PRIORITY FILING DATE: 2003-01-24
PRIORITY APPLICATION NUMBER: US 60/351,572
PRIORITY FILING DATE: 2002-01-24
PRIORITY APPLICATION NUMBER: US 09/966,614
PRIORITY FILING DATE: 2001-09-27
PRIORITY APPLICATION NUMBER: US 60/238,054
PRIORITY FILING DATE: 2000-10-05
PRIORITY APPLICATION NUMBER: US 10/281,094
PRIORITY FILING DATE: 2002-10-25
PRIORITY APPLICATION NUMBER: US 60/347,815
PRIORITY FILING DATE: 2001-10-29
PRIORITY APPLICATION NUMBER: US 10/076,535
PRIORITY FILING DATE: 2002-02-15
PRIORITY APPLICATION NUMBER: US 60/269,440
PRIORITY FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 136
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 101
LENGTH: 396
TYPE: PRT
ORGANISM: Homo sapiens
US-10-410-764-101

Query Match 95.5%; Score 2054; DB 15; Length 396;
Best Local Similarity 99.0%; Pred. No. 1.3e-145;
Matches 388; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MGANTSRRKPPVFDENEDVNFDFHFEILRAIGKSGFGKVCIVQKNDTKKMYAMKYNKQKCV 60
Db 1 MGANTSRRKPPVFDENEDVNFDFHFEILRAIGKSGFGKVCIVQKNDTKKMYAMKYNKQKCV 60

Qy 61 ERNEVRNVFKELQIMQGLEHPLVNLWYSFQDEEDMFVVDLLGGDLRVHLQONVHFKE 120
Db 61 ERNEVRNVFKELQIMQGLEHPLVNLWYSFQDEEDMFVVDLLGGDLRVHLQONVHFKE 120

Qy 121 ETVKLFICELVMALDYLNQRIIHRDMKPDNILLDEGHVHITDFNIAAMLPRQTQITTM 180
Db 121 ETVKLFICELVMALDYLNQRIIHRDMKPDNILLDEGHVHITDFNIAAMLPRQTQITTM 180

Qy 181 AGTKPYMAPENFSSRKAGAGYFAVDWMSLGVATYELLGRRPYHRSSTSSKEIVHTFET 240
Db 181 AGTKPYMAPENFSSRKAGAGYFAVDWMSLGVATYELLGRRPYHRSSTSSKEIVHTFET 240

Qy 241 TVVTYPSAWSQEMVSLKLLKLEPNPDQSFQSDVQNFPPYNDINWDVAFQKRLIPGFI 300
Db 241 TVVTYPSAWSQEMVSLKLLKLEPNPDQSFQSDVQNFPPYNDINWDVAFQKRLIPGFI 300

Qy 300 1 MGANTSRRKPPVFDENEDVNFDFHFEILRAIGKSGFGKVCIVQKNDTKKMYAMKYNKQKCV 60
Db 300 1 MGANTSRRKPPVFDENEDVNFDFHFEILRAIGKSGFGKVCIVQKNDTKKMYAMKYNKQKCV 60

Qy 61 ERNEVRNVFKELQIMQGLEHPLVNLWYSFQDEEDMFVVDLLGGDLRVHLQONVHFKE 120
Db 61 ERNEVRNVFKELQIMQGLEHPLVNLWYSFQDEEDMFVVDLLGGDLRVHLQONVHFKE 120

Qy 121 ETVKLFICELVMALDYLNQRIIHRDMKPDNILLDEGHVHITDFNIAAMLPRQTQITTM 180
Db 121 ETVKLFICELVMALDYLNQRIIHRDMKPDNILLDEGHVHITDFNIAAMLPRQTQITTM 180

Qy 181 AGTKPYMAPENFSSRKAGAGYFAVDWMSLGVATYELLGRRPYHRSSTSSKEIVHTFET 240
Db 181 AGTKPYMAPENFSSRKAGAGYFAVDWMSLGVATYELLGRRPYHRSSTSSKEIVHTFET 240

Qy 241 TVVTYPSAWSQEMVSLKLLKLEPNPDQSFQSDVQNFPPYNDINWDVAFQKRLIPGFI 300
Db 241 TVVTYPSAWSQEMVSLKLLKLEPNPDQSFQSDVQNFPPYNDINWDVAFQKRLIPGFI 300

Qy 301 NKGLNCDPTFELEEMILESPLHKKKRLAKKEKDMRKCDSSQTCLLQEHLDVQKEFI 360
Db 301 NKGLNCDPTFELEEMILESPLHKKKRLAKKEKDMRKCDSSQTCLLQEHLDVQKEFI 360

RESULT 10
US-10-254-869-2
Sequence 2, Application US/10254869
Publication No. US20030027307A1
GENERAL INFORMATION:
APPLICANT: YE, Jane et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CL001160DIV
CURRENT APPLICATION NUMBER: US/10/254,869
CURRENT FILING DATE: 2002-09-26
NUMBER OF SEQ ID NOS: 8

Db 301 NKGLNCDPTFELEEMILESPLHKKKRLAKKEKDMRKCDSSQTCLLQEHLDVQKEFI 360
Qy 361 IFNREKVNDRPNKRPQNLALAEQTKDPQVNGQ 392
Db 361 IFNREKVNDRPNKRPQNLALAEQTKDPQVNGQ 392

RESULT 9
US-09-801-876B-2
Sequence 2, Application US/09801876B
Patent No. US20020127683A1
GENERAL INFORMATION:
APPLICANT: YE, Jane et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CL001160
CURRENT APPLICATION NUMBER: US/09/801,876B
CURRENT FILING DATE: 2001-03-09
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 396
TYPE: PRT
ORGANISM: Human
US-09-801-876B-2

Query Match 95.2%; Score 2047; DB 9; Length 396;
Best Local Similarity 98.7%; Pred. No. 4.3e-145;
Matches 387; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MGANTSRRKPPVFDENEDVNFDFHFEILRAIGKSGFGKVCIVQKNDTKKMYAMKYNKQKCV 60
Db 1 MGANTSRRKPPVFDENEDVNFDFHFEILRAIGKSGFGKVCIVQKNDTKKMYAMKYNKQKCV 60

Qy 61 ERNEVRNVFKELQIMQGLEHPLVNLWYSFQDEEDMFVVDLLGGDLRVHLQONVHFKE 120
Db 61 ERNEVRNVFKELQIMQGLEHPLVNLWYSFQDEEDMFVVDLLGGDLRVHLQONVHFKE 120

Qy 121 ETVKLFICELVMALDYLNQRIIHRDMKPDNILLDEGHVHITDFNIAAMLPRQTQITTM 180
Db 121 ETVKLFICELVMALDYLNQRIIHRDMKPDNILLDEGHVHITDFNIAAMLPRQTQITTM 180

Qy 181 AGTKPYMAPENFSSRKAGAGYFAVDWMSLGVATYELLGRRPYHRSSTSSKEIVHTFET 240
Db 181 AGTKPYMAPENFSSRKAGAGYFAVDWMSLGVATYELLGRRPYHRSSTSSKEIVHTFET 240

Qy 241 TVVTYPSAWSQEMVSLKLLKLEPNPDQSFQSDVQNFPPYNDINWDVAFQKRLIPGFI 300
Db 241 TVVTYPSAWSQEMVSLKLLKLEPNPDQSFQSDVQNFPPYNDINWDVAFQKRLIPGFI 300

Qy 301 NKGLNCDPTFELEEMILESPLHKKKRLAKKEKDMRKCDSSQTCLLQEHLDVQKEFI 360
Db 301 NKGLNCDPTFELEEMILESPLHKKKRLAKKEKDMRKCDSSQTCLLQEHLDVQKEFI 360

RESULT 10
US-10-254-869-2
Sequence 2, Application US/10254869
Publication No. US20030027307A1
GENERAL INFORMATION:
APPLICANT: YE, Jane et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CL001160DIV
CURRENT APPLICATION NUMBER: US/10/254,869
CURRENT FILING DATE: 2002-09-26
NUMBER OF SEQ ID NOS: 8
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Human
US-10-254-869-2

Query Match      95.2%; Score 2047; DB 14; Length 396;
Best Local Similarity 98.7%; Pred. No. 4.3e-145;
Matches 387; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MGANTSRRPPVFDENEDVNFDFEILRAIGKSGFGKVCIVQKNDTKKMYAMKYNKQCV 60
Db |||||
Qy 1 MGANTSRRPPVFDENEDVNFDFEILRAIGKSGFGKVCIVQKNDTKKMYAMKYNKQCV 60
Db |||||
Qy 61 ERNEVRNVFKELQIMQGLEHPLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKE 120
Db |||||
Qy 61 ERNEVRNVFKELQIMQGLEHPLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKE 120
Db |||||
Qy 121 ETVKLFICELVMALDYLNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTM 180
Db |||||
Qy 181 AGTKPYMAPEMFSSRKAGYSFAVDWWSLGVTAVELLRGRPPYHRSSTSSKEIVHPTET 240
Db |||||
Qy 181 AGTKPYMAPEMFSSRKAGYSFAVDWWSLGVTAVELLRGRPPYHRSSTSSKEIVHPTET 240
Db |||||
Qy 241 TVVTYPSAWSQEMVSLKLLKLEPNPDQRFSDVQNFPPYNDINWDVAFQKRLIPGPIP 300
Db |||||
Qy 241 TVVTYPSAWSQEMVSLKLLKLEPNPDQRFSDVQNFPPYNDINWDVAFQKRLIPGPIP 300
Db |||||
Qy 301 NKGRNLCDPTFELEEMILESPLHKKKRLAKKEMKDKCDSSQTCLLQEHLDVSQKEFI 360
Db |||||
Qy 361 IFNREKVNDRDNKQPNALAEQTKDPQVINGQ 392
Db |||||
Qy 361 IFNREKVNDRDNKQPNALAEQTKDPQVINGQ 392
Db |||||

RESULT 11
US-10-667-442-2
; Sequence 2, Application US/10667442
; Publication No. US20040043466A1
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CLO01160DIV II
; CURRENT APPLICATION NUMBER: US/10/667,442
; CURRENT FILING DATE: 2003-09-23
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-667-442-2

Query Match      95.2%; Score 2047; DB 15; Length 396;
Best Local Similarity 98.7%; Pred. No. 4.3e-145;
Matches 387; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MGANTSRRPPVFDENEDVNFDFEILRAIGKSGFGKVCIVQKNDTKKMYAMKYNKQCV 60
Db |||||
Qy 61 ERNEVRNVFKELQIMQGLEHPLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKE 120
Db |||||
Qy 61 ERNEVRNVFKELQIMQGLEHPLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKE 120
Db |||||
Qy 121 ETVKLFICELVMALDYLNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTM 180
Db |||||

RESULT 12
US-10-108-260A-267A
; Sequence 267A, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1el full length cDNA
; FILE REFERENCE: HI-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 267A
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-108-260A-267A

Query Match      84.9%; Score 1827; DB 15; Length 358;
Best Local Similarity 100.0%; Pred. No. 1.1e-128;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGANTSRRPPVFDENEDVNFDFEILRAIGKSGFGKVCIVQKNDTKKMYAMKYNKQCV 60
Db |||||
Qy 61 ERNEVRNVFKELQIMQGLEHPLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKE 120
Db |||||
Qy 61 ERNEVRNVFKELQIMQGLEHPLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKE 120
Db |||||
Qy 121 ETVKLFICELVMALDYLNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTM 180
Db |||||
Qy 181 AGTKPYMAPEMFSSRKAGYSFAVDWWSLGVTAVELLRGRPPYHRSSTSSKEIVHPTET 240
Db |||||
Qy 181 AGTKPYMAPEMFSSRKAGYSFAVDWWSLGVTAVELLRGRPPYHRSSTSSKEIVHPTET 240
Db |||||
Qy 241 TVVTYPSAWSQEMVSLKLLKLEPNPDQRFSDVQNFPPYNDINWDVAFQKRLIPGPIP 300
Db |||||
Qy 241 TVVTYPSAWSQEMVSLKLLKLEPNPDQRFSDVQNFPPYNDINWDVAFQKRLIPGPIP 300
Db |||||
Qy 301 NKGRNLCDPTFELEEMILESPLHKKKRLAKKEMKDKCDSSQ 344
Db |||||
Qy 301 NKGRNLCDPTFELEEMILESPLHKKKRLAKKEMKDKCDSSQ 344
Db |||||

RESULT 13
US-10-074-978A-158
; Sequence 158, Application US/10074978A
; Publication No. US20040010119A1
; GENERAL INFORMATION:
; APPLICANT: Leite, Mario
```

```

; APPLICANT: Spytek, Kimberly A
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Fernandes, Elma
; APPLICANT: Li, Li
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Liu, Xiaohong
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ferenc
; APPLICANT: Patturajan, Meera
; APPLICANT: Bialock, Angela
; APPLICANT: Ballinger, Robert
; APPLICANT: Vernet, Corine
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Gusev, Vladimir
; APPLICANT: Rastelli, Luca
; APPLICANT: Mezes, Peter S
; APPLICANT: Ellerman, Karen
; APPLICANT: Heyes, Melvin P
; APPLICANT: Herrman, John
; APPLICANT: Pena, Carol E A
; APPLICANT: Shimkets, Richard A
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Moore, No. US20040010119A11le
; APPLICANT: Shenoy, Suresh
; APPLICANT: Edinger, Shlomit
; APPLICANT: Gunther, Erik
; APPLICANT: Stone, Dave
; APPLICANT: Millet, Isabelle
; APPLICANT: Payman, John
; APPLICANT: Smithson, Glenda
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-269
; CURRENT APPLICATION NUMBER: US/10/074,978A
; CURRENT FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: 60/268,221
; PRIOR FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/335,109
; PRIOR FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: 60/312,284
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: 60/268,496
; PRIOR FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 60/276,703
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/330,293
; PRIOR FILING DATE: 2001-10-18
; PRIOR APPLICATION NUMBER: 60/322,127
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/280,899
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 60/310,797
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/268,646
; PRIOR FILING DATE: 2001-02-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 158
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Mus musculus
; US-10-074-978A-158

Query Match      67.0%; Score 1441; DB 15; Length 414;
Best Local Similarity 68.3%; Pred. No. 1.1e-99;
Matches 280; Conservative 43; Mismatches 71; Indels 16; Gaps 4;

Qy 1 MGANTSRRKPPVFDENEDVDFHFEILRAIGKSGFGKVCIVQKNDTKKMYAMKYNKQKCV 60
Db 1 MGGNHSKPPVFDENEENVDHFDHILRAIGKSGFGKVCIVQKNDTKKMYAMKYNKQKCV 60
Qy 61 ERNEVRNVFRELQIMOGLEHPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFK 120
Qy 1 MGANTSRRKPPVFDENEDVDFHFEILRAIGKSGFGKVCIVQKNDTKKMYAMKYNKQKCV 60
Db 1 MGGNHSKPPVFDENEENVDHFDHILRAIGKSGFGKVCIVQKNDTKKMYAMKYNKQKCV 60
Qy 61 ERNEVRNVFRELQIMOGLEHPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFK 119
Db 61 QSRDEVRNVFRELQIMOGLEHPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFT 120
Qy 120 EETVKLFICELVMDYLQNRRIHRDMKPDNILLDEGHVHITDFNIAAMLPRETQTT 179
Db 121 EGTVKLYICELALALEYLQRYHIIHRDIKPDNILLDEGHVHITDFNIAATVLKSEKASS 180
Qy 180 MAGTKPYMAPEMPS--SRKAGAGYSPAVDWSLGVATAYELLGRPRPYHRSSTSSKEIVHT 237
Db 181 MAGTKPYMAPPEVTVQVYVDDGGPGYSYPVDWMSLGVATAYELLGRWPRPYHRSATPIDEILNM 240
Qy 238 FETTVTVPSAWSQEMVSLKLLLEPNPDORFSDVQNPFPYMNNDINWDAVFOKRLIPG 297
Db 241 FKVERVHYSWTCEGWSLKKLLTKDPESRLSLRDIQSWTYLADNWDNDAVFEKALMPG 300
Qy 298 FIPNKGRLNCDPTFELEEMILESPLHKKKKRLAK--KEKDMRKCDSSQTCLLQEHLDVSQK 356
Db 301 FVFNKGRLNCDPTFELEEMILESPLHKKKKRLAKHRSRSTKDCSCLNGHLQOCLETVR 360
Qy 357 KEFIIFNREKVNDRFNKQPNLALAEQTKDPQVT--NQMDTGLSETTQTSK 405

; APPLICANT: YE, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001160
; CURRENT APPLICATION NUMBER: US/09/801,876B
; CURRENT FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 404
; TYPE: PRT
; ORGANISM: Mus Musculus
; US-09-801-876B-4

Query Match      66.5%; Score 1430.5; DB 9; Length 404;
Best Local Similarity 68.1%; Pred. No. 6.5e-99;
Matches 280; Conservative 43; Mismatches 71; Indels 17; Gaps 5;

Qy 1 MGANTSRRKPPVFDENEDVDFHFEILRAIGKSGFGKVCIVQKNDTKKMYAMKYNKQKCV 60
Db 1 MGGNHSKPPVFDENEENVDHFDHILRAIGKSGFGKVCIVQKNDTKKMYAMKYNKQKCV 60
Qy 61 -ERNEVRNVFRELQIMOGLEHPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFK 119
Db 61 QSRDEVRNVFRELQIMOGLEHPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFT 120
Qy 120 EETVKLFICELVMDYLQNRRIHRDMKPDNILLDEGHVHITDFNIAAMLPRETQTT 179
Db 121 EGTVKLYICELALALEYLQRYHIIHRDIKPDNILLDEGHVHITDFNIAATVLKSEKASS 180
Qy 180 MAGTKPYMAPEMPS--SRKAGAGYSPAVDWSLGVATAYELLGRPRPYHRSSTSSKEIVHT 237
Db 181 MAGTKPYMAPPEVTVQVYVDDGGPGYSYPVDWMSLGVATAYELLGRWPRPYHRSATPIDEILNM 240
Qy 238 FETTVTVPSAWSQEMVSLKLLLEPNPDORFSDVQNPFPYMNNDINWDAVFOKRLIPG 297
Db 241 FKVERVHYSWTCEGWSLKKLLTKDPESRLSLRDIQSWTYLADNWDNDAVFEKALMPG 300
Qy 298 FIPNKGRLNCDPTFELEEMILESPLHKKKKRLAK--KEKDMRKCDSSQTCLLQEHLDVSQK 356
Db 301 FVFNKGRLNCDPTFELEEMILESPLHKKKKRLAKHRSRSTKDCSCLNGHLQOCLETVR 360
Qy 357 KEFIIFNREKVNDRFNKQPNLALAEQTKDPQVT--NQMDTGLSETTQTSK 405

RESULT 14
US-09-801-876B-4
; Sequence 4, Application US/09801876B
; Patent No. US20020127683A1
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001160
; CURRENT APPLICATION NUMBER: US/09/801,876B
; CURRENT FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 404
; TYPE: PRT
; ORGANISM: Mus Musculus
; US-09-801-876B-4

Db 61 ERDEVRNVFRELQIMOGLEHPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHTE 120
Qy 121 ETVKLFICELVMDYLQNRRIHRDMKPDNILLDEGHVHITDFNIAAMLPRETQITM 180
Db 121 GTVKLYICELALALEYLQRYHIIHRDIKPDNILLDEGHVHITDFNIAATVLKSEKASSM 180
Qy 181 AGTKPYMAPEMPS--SRKAGAGYSPAVDWSLGVATAYELLGRPRPYHRSSTSSKEIVHTF 238
Db 181 AGTKPYMAPPEVTVQVYVDDGGPGYSYPVDWMSLGVATAYELLGRWPRPYHRSATPIDEILNMF 240
Qy 239 ETTTVTVPSAWSQEMVSLKLLLEPNPDORFSDVQNPFPYMNNDINWDAVFOKRLIPGF 298
Db 241 KVERVHYSWTCEGWSLKKLLTKDPESRLSLRDIQSWTYLADNWDNDAVFEKALMPGF 300
Qy 299 IPNKGRLNCDPTFELEEMILESPLHKKKKRLAK--KEKDMRKCDSSQTCLLQEHLDVSQK 357
Db 301 VFNKGRLNCDPTFELEEMILESPLHKKKKRLAKHRSRSTKDCSCLNGHLQOCLETVRK 360
Qy 358 EFTIFNREKVNDRFNKQPNLALAEQTKDPQVT--NQMDTGLSETTQTSK 405
Db 361 EFTIFNREKLRR-----QQHGDGQLSDLDGRIGSQTSKLDQGR 399
```

[illegible]

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OM protein - protein search, using sw model

Run on: December 17, 2004, 09:25:19 ; Search time 39 Seconds
(without alignments)
1004.108 Million cell updates/sec

Title: US-10-620-845-9
Perfect score: 2151
Sequence: 1 MGANTSRRKPPVEDENEDVNF.....VTNGQMDTGLSEFTQTSKVS 407

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: Pir1.*
2: Pir2.*
3: Pir3.*
4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	852.5	39.6	379	2 T23688	hypothetical prote
2	546	25.4	479	2 A38578	protein kinase 2 (
3	537.5	25.0	648	1 JQ1150	protein kinase (EC
4	534	24.8	480	2 S56639	ribosomal protein
5	529.5	24.6	465	2 S68462	protein kinase ATP
6	526	24.5	680	2 S37955	protein kinase YPK
7	521.5	24.2	353	2 C31751	protein kinase (EC
8	521	24.2	471	2 S68463	protein kinase ATP
9	519.5	24.2	696	2 S55694	protein kinase (EC
10	519.5	24.2	785	2 T20232	hypothetical prote
11	518	24.1	352	2 S19027	protein kinase A (
12	517	24.0	359	2 T21211	hypothetical prote
13	514.5	23.9	823	2 S48956	ribosomal protein
14	514.5	23.9	740	2 S48956	probable protein k
15	514	23.9	375	2 T21212	hypothetical prote
16	514	23.9	677	2 JS0178	protein kinase YKR
17	513.5	23.9	351	1 OKHYCA	protein kinase (EC
18	513.5	23.9	733	2 A57459	ribosomal protein
19	512.5	23.8	360	1 OKHUGC	protein kinase (EC
20	510	23.7	359	1 OKKW1	protein kinase (EC
21	509.5	23.7	351	1 OKHUC2	protein kinase (EC
22	509.5	23.7	351	1 OKRT2C	protein kinase (EC
23	508.5	23.6	586	2 A53758	protein kinase C (
24	508.5	23.6	587	2 A49509	protein kinase C (
25	507.5	23.6	351	1 OKBO3C	protein kinase (EC
26	507.5	23.6	752	1 A32571	ribosomal protein
27	507	23.6	351	1 OKHYCB	protein kinase (EC
28	507	23.6	351	1 OKWSCB	protein kinase (EC
29	507	23.6	351	1 OKRTCB	protein kinase (EC

ALIGNMENTS

RESULT 1

T23688
hypothetical protein M03C11.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T23688
R:McMurray, A.
submitted to the EMBL Data Library, April 1995
A:Reference number: Z19783
A:Accession: T23688
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-379 <WIL>
A:Cross-references: UNIPROT:Q21483; EMBL:Z49128; PIDN:CAA88953.1; GSPDB:GN00021; CESP:MO
C:Genetics:
A:Gene: CESP:M03C11.1
A:Map position: 3
A:Introns: 41/3; 67/3; 96/3; 127/2; 240/3; 299/2; 358/3
C:Superfamily: kinase-related transforming protein; protein kinase homology

Query Match	39.6%	Score	852.5	DB 2	Length	379	
Best Local Similarity	44.4%	Pred. No.	5.2e-31	Indels	13	Gaps	4
Matches	159	Conservative	70	Mismatches	116		
Qy	22	HPEILRAIGSGFKVCIVQKNDTKQYAMKYNKQKCVNERVNYFKEIQIMQGLEHP	81				
Db	27	HFSVIRSIGRGAGFKVCIVQERTKKYFALKYMNKGRCEIBKGAANVIRELTLLSKMSHP	86				
Qy	82	FLVNLWYSFQDEBDMFVVDLLGGDLRYHLQONVHFKEETVKLFICELVMALDYLNQR	141				
Db	87	FIVNLWYTFQGDGYVMVSDLLGGDLRYHLQONVHFKEETVKLFICELVAYELHEMK	146				
Qy	142	IIHRDMKPNILLDEGHVHTIDFNIAAMLPRETQITTMAGTKPYMAPEMFSS--RKAG	199				
Db	147	IVHRDIKPNILLDEQCHALRTDLNLATQLEDQLATSYSGTRPYMAPEIYATLEIDG	206				
Qy	200	YSPAVDWSLGVYAYELLGRRRYHRSSTSSKEIVHTFTTVPVYPSANSQEMVSLKK	259				
Db	207	YDSRVDWALGVCFEYMLRGRTPEFSSRTPKEAYVAFRESSIPYPAHPTDILQIFNS	266				
Qy	260	LLEPNPDQRFSQLSDVQNFPMYNDINMDAVFQKRLIPGFI PNKGRNLCDPTFELEEMILE	319				
Db	267	MLKFDKEKRLVGLAEIKKHSYTERIDPKSVFEKKPSVPFIPCKEGLNCDPMYLEERILV	326				
Qy	320	SKPLHKKKKRLAKKEDKMDKRCDSQTLQEHLDSDVQKEFIIPNREKVNDRDNKRQPN	377				
Db	327	STPIH--RRRTNHNSSGRSSSPQNAALVE----VSKAFIDFSRHNV-----KIEPN	373				

RESULT 2

A38578

protein kinase 2 (EC 2.7.1.1) - slime mold (Dictyostelium discoideum)
C:Species: Dictyostelium discoideum
C:Date: 28-Feb-1992 #sequence_revision 28-Feb-1992 #text_change 09-Jul-2004
R:Accession: A38578
R:Haribabu, B.; Dotti, R.P.
Proc. Natl. Acad. Sci. U.S.A. 88, 1115-1119, 1991
A:Title: Identification of a protein kinase multigene family of Dictyostelium discoideum
A:Reference number: A38578; MUID:91142122; PMID:11996312
A:Accession: A38578
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-479 <HAR>
A:CROSS-references: UNIPROT:P28178; GB:M59744; NID:g167717; PID:AA33186.1; PID:g167718
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog
C:Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; serine/threonine
F:151-407/Domain: protein kinase homology <KIN>
F:159-167/Region: protein kinase ATP-binding motif

Query Match 25.4%; Score 546; DB 2; Length 479;
Best Local Similarity 36.5%; Pred. No. 1.6e-17;
Matches 118; Conservative 66; Mismatches 123; Indels 16; Gaps 6;

Qy 11 VFEDN-EDVNFDFEILRAIGKSGFKVCIVQKNDTKMYAMKYNKQKCVNERVNVF 69
Db 140 IFSKNQKQATKDDPELLNVIGKSGFKYQVKKKGEDKIFAMKVLKDAIIRKQVNHK 199
Qy 70 KQLQIMQGLEHPFLVNLWYSFQDEDMFVVDLLGLDLRLHLOQNVHFKEETVKLFICE 129
Db 200 SEKITLQICSHFFIVNLHYAQTQDKLYWLDVFNGBELFHLKRGESPRVKIYAAE 259
Qy 130 LVMALDYLNQRIIHRDMKPNILLDEHGHVHTIDFNIAAMLPRETQITTMAGTKPYMAP 189
Db 260 IVSALDHLHKQDIVYRDLKPNILLDSGHICITDFGLSKKIETTDGTFTCGTPPEYLAP 319
Qy 190 EMFSRKAGYSPAVDWMSLGVATYELLGRPRPHIRSSSTSKSEIVHTFTTVPVPSAW 249
Db 320 EVLN---GHGHCAGVDWMSLGLTYEMLTGLPPFYQNVSTMYQKILNGELKIPTY---I 373
Qy 250 SOEMVSLKLLPEPNDFQSFQSL---SDVQNPYPYNDINWDVFOKRLIPGPFP---NKG 303
Db 374 SPEAKSLLEGLLTREVDKRLGTGGGEVQKQHPFNKIDWEKLDKREVEVHFKPKVKSSTD 433
Qy 304 RLNCDDPTPELE---EMILESRLP 323
Db 434 ISQIDPVFTQSRPMDSLVETSAL 456

RESULT 3
JQ1150
protein kinase (EC 2.7.1.37) CAMP-dependent, catalytic chain - slime mold (Dictyostelium
C:Species: Dictyostelium discoideum
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C:Accession: JQ1150
R:Busker, E.; Anjard, C.; Scholder, J.C.; Raymond, C.D.
Gene 102, 57-65, 1991
A:Title: Isolation of two genes encoding putative protein kinases regulated during Dicty
A:Reference number: JQ1150; MUID:91323730; PMID:1864510
A:Accession: JQ1150
A:Molecule type: DNA
A:Residues: 1-648 <HUB>
A:CROSS-references: UNIPROT:P34099; GB:M38703
C:Genetics:
A:Gene: PK2
A:Introns: 578/3
C:Complex: heterodimer with regulatory chain; active catalytic chain is released when cAMP
C:Function:
A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine
A>Note: important for cell type differentiation and fruiting body morphogenesis
C:Superfamily: Dictyostelium CAMP-dependent protein kinase catalytic chain; protein kinase
C:Keywords: ATP; magnesium; phosphoprotein; phosphotransferase; serine/threonine-specific
F:126-223/Region: glutamine-rich
F:297-312/Region: glutamine-rich
F:334-590/Domain: protein kinase homology <KIN>

F:342-350/Region: protein kinase ATP-binding motif
F:365,384,459,461/Active site: Lys, Glu, Asp, Lys #status predicted
F:464,468/Binding site: magnesium (Asn, Asp) #status predicted

Query Match 25.0%; Score 537.5; DB 1; Length 648;
Best Local Similarity 34.1%; Pred. No. 5e-17;
Matches 109; Conservative 74; Mismatches 120; Indels 17; Gaps 6;

Qy 9 PPVFEDENEDVNFDFEILRAIGKSGFKVCIVQKNDTKMYAMKYNKQKCVNERVNVF 68
Db 325 PPV---NARELKEFKQIRVLGTGTFGKVLQNTKQGCYAMKCLAKAYVQLQKVEHL 381
Qy 69 FKELQIMQGLEHPFLVNLWYSFQDEDMFVVDLLGLDLRLHLOQNVHFKEETVKLFICE 128
Db 382 NSEKILLSIHHPPIVNLVYQAFQDEKKLYLLFEVAGGEVFTHLRKSMSKFSNSTAKFYAA 441
Qy 129 ELVMALDYLNQRIIHRDMKPNILLDEHGHVHTIDFNIAAMLPRETQITTMAGTKPYMA 188
Db 442 EIVLALDFLHKQNIYRDLKPNILLDNQGHKIKITDFGAKRV---EDRTFTLCGTPEYLA 499
Qy 189 PEMFSRKAGYSPAVDWMSLGVATYELLGRPRPHIRSSSTSKSEIVHTFTTVPVPSA 248
Db 500 PEIIQSK---GHGKAVDWMSLGLIIFELMAGYPPFY---DDDTFALYNKILAGRITPLG 553
Qy 249 WSQEMVSLKLLPEPNDFQSFQSL---DVQNPYPYNDINWDVFOKRLIPGPFPKNGR 304
Db 554 FVDVAKDLIKRLLTADTRRLGALKDQALDVGNHRWFSNDINWERLYQRRDNGPPIPKIQH 613
Qy 305 LNCDDPTPELE---EMILESRLP 322
Db 614 QGDSNPFMYDEEMVEEPP 633

RESULT 4
S56639
ribosomal protein S6 kinase homolog (clone Asp11) - oat
N:Alternate names: mitogen-activated protein kinase pp70 homolog
C:Species: Avena sativa (Oat)
C:Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 16-Aug-2004
C:Accession: S56639
R:Huttly, A.K.; Phillips, A.L.
Plant Mol. Biol. 27, 1043-1052, 1995
A:Title: Gibberellin-regulated expression in oat aleurone cells of two kinases that show
A:Reference number: S56638; MUID:95284341; PMID:7766874
A:Accession: S56639
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-480 <HUT>
A:CROSS-references: UNIPROT:Q43380; EMBL:X79992; NID:g871985; PIDN:CAA56313.1; PID:g8719
C:Superfamily: protein kinase homolog
C:Keywords: ATP; phosphotransferase; protein kinase
F:149-407/Domain: protein kinase homology <KIN>
F:157-165/Region: protein kinase ATP-binding motif

Query Match 24.8%; Score 534; DB 2; Length 480;
Best Local Similarity 36.0%; Pred. No. 5.5e-17;
Matches 109; Conservative 61; Mismatches 123; Indels 10; Gaps 3;

Qy 14 ENEDVNFDFEILRAIGKSGFKVCIVQKNDTKMYAMKYNKQKCVNERVNVFKEQLQ 73
Db 142 ENEAVGLDNFVLKLVQGGAGFYQVRMKGTSIIYAMKVRKDKILEKNHAEYMKAEKD 201
Qy 74 IMQGLEHPFLVNLWYSFQDEDMFVVDLLGLDLRLHLOQNVHFKEETVKLFICEYMA 133
Db 202 ILTKVDHPFVQLRYSFQTKYRLVLDVFNNGHLPFLYQOGLFRELARIYTAIEVSA 261
Qy 134 LDYLNQRIIHRDMKPNILLDEHGHVHTIDFNIAAMLPRETQITTMAGTKPYMAPNFS 193
Db 262 VAHLHANGIMHRDLKPNILLDARGHAMLTDFGLAKEFDENTRSNMGCTVEYMAPEIV- 320
Qy 194 SRKAGYSPAVDWMSLGVATYELLGRPRPHIRSSSTSKSEIVHTFTTVPVPSAQSEM 253
Db 321 --QGRGHDKAADWMSVIGILLFEMLTGKPPFF---GGNRDKIQQKIVREKMKLPSYLSSEV 375

Qy 254 VSLKKLLEPNPDQRFSSQ----LSDVQNFPPYMNNDINWDVAFQKRLIPGFIPIKNGRLNCDP 309
Db 376 HSLKGLLHKGAKRGLSGSGSDEIKRHKWFKAVNWKRLERQIQSPFCNVAQQTCTA 435
Qy 310 TFE 312
Db 436 NFD 438

RESULT 5
S68462
protein kinase ATPK6/ATPK1 (EC 2.7.1.1) - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 05-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 16-Aug-2004
C;Accession: S68462; A54141
R;Mizoguchi, T.; Hayashida, N.; Yamaguchi-Shinozaki, K.; Kamada, H.; Shinozaki, K.
FEBS Lett. 358, 199-204, 1995
A;Title: Two genes that encode ribosomal-protein S6 kinase homologs are induced by cold
A;Reference number: S68462; MUID:95129712; PMID:7828736
A;Accession: S68462
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-465 <MIZ>
A;Cross-references: UNIPROT:P42818; EMBL:D42056; NID:g667996; PIDN:BAA07656.1; PID:dl1008
R;Zhang, S.H.; Lawton, M.A.; Hunter, T.; Lamb, C.J.
J. Biol. Chem. 269, 17586-17592, 1994
A;Title: atpki, a novel ribosomal protein kinase gene from Arabidopsis. I. Isolation, ch
A;Reference number: A54141; MUID:94292519; PMID:7912697
A;Contents: ecotype Landsberg erecta
A;Accession: A54141
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-465 <ZHA>
A;Cross-references: GB:I29030; NID:g508307; PIDN:AAA21142.1; PID:g508308
A;Note: sequence extracted from NCBI backbone (NCBIN:149344, NCBI:P:149415)
C;Superfamily: protein kinase homolog
C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F;132-389/Domain: protein kinase homolog <KIN>
F;140-148/Region: protein kinase ATP-binding motif

Query Match 24.6%; Score 529.5; DB 2; Length 465;
Best Local Similarity 34.8%; Pred. No. 8.4e-17;
Matches 104; Conservative 65; Mismatches 119; Indels 11; Gaps 3;

Qy 18 VNFDFHILRAIGSGFGKVCIVQKNTKQMYAMKQKQKVERNEVRNVFKELQIMQG 77
Db 129 VGIDDFVMKVVGKAGFKVQVRKXETSEIYAMKWKDKHIMEKNAEYMKAEERDILTK 188
Qy 78 LEHPPFLNLYSFQDEEDMFVVDLLGGDLRYHLQQNVHFKETVKLFIQELVMAHDYL 137
Db 189 IDHPFFIVQLKYSFQTKYRLYLVLDFINGGHLFFQLYHQGLFREDLARVYTAIEIVSAVSHL 248
Qy 138 QNQRRIHRDMKPDNILLDEGHVHITDPNIAAMLPRETOITTMAGTKPYMAPFMFSSRKG 197
Db 249 HEKIMARDLAPENILMDTDGHWMLTDPLGAKFEENTRSNMGCTTEYMAPEIV---RG 305
Qy 198 AGYSFVDWWSLGYATAYELLRGRPYHRSSTSSKEIVHTFETTVTPVTPYSAWSQEMVSL 257
Db 306 KGHDKAADWMSVGIILLYEMLTGKPFGLSGKGIQKIV---KDKIKLPQLSNEAHAIL 361
Qy 258 KLLLEPNPDQ-----FSQLSDVQNFPPYMNNDINWDVAFQKRLIPGFIPIKNGRLNCDPTE 312
Db 362 KGLLQKQEPERRLGLSGLSGAEIKQHKWFKGINWKKLEAREVMPSPFKPVSGRQCIANPD 420

RESULT 6
S37955
protein kinase YPK1 (EC 2.7.1.1) - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein YKL126W
C;Species: Saccharomyces cerevisiae
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 16-Aug-2004
C;Accession: S37955; A31248; S30903

R;Ramezani Rad, M.; Xu, G.; Kirchrath, L.; Fritz, C.; Keuchel, H.; Hollenberg, C.P.
submitted to the Protein Sequence Database, March 1994
A;Reference number: S37955
A;Accession: S37955
A;Molecule type: DNA
A;Residues: 1-680 <RAM>
A;Cross-references: UNIPROT:P12688; EMBL:Z28126; NID:g486212; PIDN:CAA81967.1; PID:g4862
A;Experimental source: strain S288C
R;Maurer, R.A.
DNA 7, 469-474, 1988
A;Title: Isolation of a yeast protein kinase gene by screening with a mammalian protein
A;Reference number: A31248; MUID:89090805; PMID:2850145
A;Accession: A31248
A;Molecule type: DNA
A;Residues: 1-200, 'L', 202-552, 'I', 554-680 <MAU>
A;Cross-references: EMBL:M21307; NID:gl72180; PIDN:AAA34880.1; PID:gl72181
R;Chen, P.; Lee, K.S.; Levin, D.E.
Mol. Gen. Genet. 236, 443-447, 1993
A;Title: A pair of putative protein kinase genes (YPK1 and YPK2) is required for cell gr
A;Reference number: S30903; MUID:93173125; PMID:8437590
A;Accession: S30903
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-200, 'L', 202-226, 'T', 228-552, 'I', 554-680 <CHE>
C;Genetics:
A;Gene: SGD:YPK1
A;Cross-references: SGD:S0001609; MIPS:YKL126w
A;Map position: 11L
C;Superfamily: protein kinase homolog
C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F;345-602/Domain: protein kinase homolog <KIN>
F;353-361/Region: protein kinase ATP-binding motif
F;470/Active site: Asp #status predicted

Query Match 24.5%; Score 526; DB 2; Length 680;
Best Local Similarity 32.6%; Pred. No. 1.7e-16;
Matches 117; Conservative 77; Mismatches 123; Indels 42; Gaps 10;

Qy 8 KPPVFDENEDVNFDFHILRAIGSGFGKVCIVQKNTKQMYAMKQKQKVERNEVRN 67
Db 335 KP---SRNKPLSIDDFLLKVGSGFKVMQVRKDTQKVYALKAKRKSYIVSKSEVTH 391
Qy 68 VFKELOIQMGLHPPFLNLYSFQDEEDMFVVDLLGGDLRYHLQQNVHFKETVKLFI 127
Db 392 TLAEITVLARVDCFFIVPLKFSQSPKLYFVLAFINGGELFYHLQKREGFDLSRRARYT 451
Qy 128 CELVWALDYQNQRRIHRDMKPDNILLDEGHVHITDPNIAAMLPRETOIT-TMAGTKPY 186
Db 452 AELLCALDNLHLKLDVVYRDLPENILLDYQGHIALCDFGLCKLNKDDKDTDTFCGTPEY 511
Qy 187 MAPFMFSSRKGAGYSFVDWWSLGYATAYELLRGRPYHRSSTSSKEIVHTFETTV---V 243
Db 512 LAPELL---LGLGYTKAVDWMTLGLVLYEMLTGLPPYV-----DEDVPMVKKILQSP 562
Qy 244 TYPYSAWSQEMVSLKLLLEPNPDQ---FSQLSDVQNFPPYMNNDINWDVAFQKRLIPGFI 301
Db 563 VFPDGFDRADKDLIGLLSLRDPTRRLGYNGADEIRNHPFFSQLSWKRLMKGYIPPYKPA 622
Qy 302 KGRNLNCDPTELEBEMILESPLHKKKRLAKKEDKMKCDSSQTCLLQEHLL-DSVQKEF 359
Db 623 VS--NSMDTSNFDDEFTREKPI-----DS---VDEYLSESVQKQF 658

RESULT 7
C31751
protein kinase (EC 2.7.1.37), CAMP-dependent, catalytic chain - fruit fly (Drosophila me
C;Species: Drosophila melanogaster
C;Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 09-Jul-2004
C;Accession: C31751; A28269
R;Kalderson, D.; Rubin, G.M.
Genes Dev. 2, 1539-1556, 1988
A;Title: Isolation and characterization of Drosophila cAMP-dependent protein kinase gene
A;Reference number: A31751; MUID:89107990; PMID:3215511

A:Accession: C31751
A:Molecule type: DNA
A:Residues: 1-353 <KAL>
A:Cross-references: UNIPROT:P12370; EMBL:X16969; NID:g7806; PIDN:CAA34840.1; PID:g7807;
R:Forster, J.L.; Higgins, G.C.; Jackson, F.R.
J. Biol. Chem. 263, 1676-1681, 1988
A:Title: Cloning, sequence, and expression of the Drosophila cAMP-dependent protein kinase
A:Reference number: A32684; MUID:88115281; PMID:2828348
A:Accession: A28269
A:Molecule type: DNA
A:Residues: 2-353 <FOS>
A:Cross-references: GB:M18655; GB:J03504; NID:g157051; PIDN:AAA28412.1; PID:g157052
C:Genetics:
A:Gene: FlyBase:PkA-C1
A:Cross-references: FlyBase:PBgn0000273
C:Superfamily: Kinase-related transforming protein; protein kinase homology
C:Keywords: ATP; blocked amino end; cAMP binding; heterotrimer; lipoprotein; magnesium
F:2-353/Product: protein kinase, cAMP-dependent, catalytic chain #status predicted <MAT>
F:44-300/Domain: protein kinase homology <KIN>
F:52-60/Region: protein kinase ATP-binding motif
F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F:2/Modified site: aspartic acid (Asn) #status predicted
F:57,58,124,130,173,186/Binding site: Mg-ATP (Phe, Glu, Glu, Thr) #status predicted
F:75,94,169,171/Active site: Lys, Glu, Asp, Lys #status predicted
F:174,187/Binding site: magnesium (Asn, Asp) #status predicted
F:200/Binding site: phosphate (Thr) (covalent) #status predicted
F:341/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 24.2%; Score 521.5; DB 2; Length 353;
Best Local Similarity 34.7%; Pred. No. 1.5e-16;
Matches 111; Conservative 73; Mismatches 117; Indels 19; Gaps 6;
QY 21 DFEITLRAIGKSGFKGKIVQKNDTKKMYAMKYNKQKVERNEVNVFKELQIMOGLEH 80
DB 44 DFERIKLTGTSFGKIVQKNDTKKMYAMKYNKQKVERNEVNVFKELQIMOGLEH 103
QY 81 PELVNLVTSFQDEDMFVMDLLGLGDLRYHLQNVHFEETVKLFCICELVMDLYLQNG 140
DB 104 PFLVSLRVHFKDNLVLYVVPVGVGEMFSLRKVGRESEHRSFYAAQIVLAPELHYL 163
QY 141 RIHRMDKPDNILLDEHGHVHTDNLNIAMLPRETQITMAGTKPYMAPFSSKKGAGY 200
DB 164 DIYRDLKPNLLDSQGYLVKVTDFGFAKRVKGR--WTLCGTPEYLAPEILSK--GY 218
QY 201 SFADVMSLGVTAELLGRRRPYHRSSTSSKEIVHTETTV---VTVPVSAWSQBMVSL 257
DB 219 NKAVDWALGVLVYEMAGYPPF-----ADQPIQVEKIVSGKVRPSPHSGDLKDL 272
QY 258 KKLLEPNPDRFSQL-----SDVQNFPMNDINNDVAFQKRLIPGIPN-KGRNLCDPTFE 312
DB 273 RNLLQVLDLTKRYGNLKAGVNDIKNQKWPASTDWIAIFOKKIEAPFIPCKGPGDTSNFD 332
QY 313 LSEMIKESPLHKKKRLAK 332
DB 333 YEEALRLISSTKCAKEFAE 352

RESULT 8
S68463
protein kinase ATPK19 (EC 2.7.1.1-) - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 05-Dec-1996 #sequence_revision 27-Feb-1997 #text_change 16-Aug-2004
C:Accession: S68463
R:Mizoguchi, T.; Hayashida, N.; Yamaguchi-Shinozaki, K.; Kamada, H.; Shinozaki, K.
FEBS Lett. 358, 199-204, 1995
A:Title: Two genes that encode ribosomal-protein S6 kinase homologs are induced by cold
A:Reference number: S68462; MUID:95129712; PMID:7828736
A:Accession: S68463
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-471 <MTZ>
A:Cross-references: UNIPROT:Q39030; EMBL:D42061; NID:g1526412; PIDN:BAA07661.1; PID:d100
C:Superfamily: protein kinase homology

C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
P:138-395/Domain: protein kinase homology <KIN>
F:146-154/Region: protein kinase ATP-binding motif

Query Match 24.2%; Score 521; DB 2; Length 471;
Best Local Similarity 34.0%; Pred. No. 2e-16;
Matches 108; Conservative 63; Mismatches 123; Indels 24; Gaps 4;
QY 12 FDSEED-----VNFDPHFILRAIGKSGFKGKIVQKNDTKKMYAMKYNKQK 58
DB 116 FSGNDTDSKSPPEVGVVGLIEDFEVLKVGQAGKVVQVRKDTSEIYAMKVMKDK 175
QY 59 CVERNEVNVFKELQIMOGLEHPEFLVNLVYSFQDEDMFVMDLLGLGDLRYHLQNVH 118
DB 176 IVEKNAEYKMAERDILTIDHPFIVQLKYSFQTKRYLYLVLDINGHILFFOLYHOG 235
QY 119 KEETVKLFCICELVMDLYLQNGRIHRDMKPDNILLDEHGHVHTDNLNIAMLPRETQIT 178
DB 236 REDLARVYTAIVSVVSHLHEKGIMHRDLPENILMDVGHVMTLDFGLAKFEENTRSN 295
QY 179 TMAGTKPYMAPENFFSRKGGAGYSFADVMSLGVTAELLGRRRPYHRSSTSSKEIVHTF 238
DB 296 SMCCTTEYMAPEIV---RGKHDKAADWSVGLLYEMLTGKPPFLGSGKGIQKIV-- 349
QY 239 ETTVTVTPVSAWSQBMVSLKLLLEPNDRF-----SOLSDVQNFPMNDINNDVAFQKRL 294
DB 350 -KDKIKLPQVFVNEAHALLKGLQKPEPRLGSGSGABEIKKHKWFKAINWKKLEAREV 408
QY 295 IPGFIPNKGRLNCDPTFE 312
DB 409 QPSFKPAVSGRQCIANFD 426

RESULT 9

S55694
Protein kinase (EC 2.7.1.37) sck1, cAMP-dependent - fission yeast (Schizosaccharomyces p
C:Species: Schizosaccharomyces pombe
C:Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 16-Aug-2004
C:Accession: S55694; T38040
R:Jin, M.; Fujita, M.; Cullley, B.M.; Apolinaro, E.; Yamamoto, M.; Maundrell, K.; Hoffma
Genetics 140, 457-467, 1995
A:Title: sck1, a high copy number suppressor of defects in the cAMP-dependent protein ki
A:Reference number: S55694; MUID:96120227; PMID:7498728
A:Accession: S55694
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-696 <JIN>
A:Cross-references: UNIPROT:P50530; GB:D38108; NID:g1136301; PIDN:BAA07286.1; PID:d10078
A:Note: the authors translated the codon GAT for residue 687 as His
R:McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.; Whitehead, S.; Churcher, C.M.
submitted to the EMBL Data Library, August 1999
A:Reference number: Z21764
A:Accession: T38040
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-176, 'F', 178-198, 'A', 200-696 <MCD>
A:Cross-references: EMBL:AL109951; PIDN:CAB53053.1; GSPDB:GN00066; SPDB:SPAC1B9.02c
A:Experimental source: strain 972h-; cosmid c1B9
C:Genetics:
A:Gene: sck1; SPDB:SPAC1B9.02c
A:Map position: 1
A:Insertions: 80/3; 311/1; 633/2
C:Superfamily: protein kinase homology
C:Keywords: ATP; phosphotransferase; protein kinase
F:300-563/Domain: protein kinase homology <KIN>
F:308-316/Region: protein kinase ATP-binding motif

Query Match 24.2%; Score 519.5; DB 2; Length 696;
Best Local Similarity 37.2%; Pred. No. 3.3e-16;
Matches 112; Conservative 63; Mismatches 111; Indels 15; Gaps 7;
QY 11 VFDEDEDVNF--DFEITLRAIGKSGFKGKIVQKNDTKKMYAMKYNKQKVERNEVNV 68
DB 112 VFDEDEDVNF--DFEITLRAIGKSGFKGKIVQKNDTKKMYAMKYNKQKVERNEVNV 68

Db 288 IYEHIEHVRYGPEDTALRLICKGTGQVYLVRKNDTNRIYAMKISKKLIVRKKEVTHT 347
Qy 69 FKEIQIMQGL---EHPFLVNLWYSFQDEEDFMVVDLLGGDLRYHLQONVHFKEETVKL 125
Db 348 LGERNIVRTSLDESPFIVGLKFSQASDLYLITDYMGGELFWHLQHEGRFPQORAKF 407
Qy 126 FICELVMAVDYLNQRIIHRDMKPDNILLDEGHVHITDFNIA-AMLPRETQITTMAGTK 184
Db 408 YIAELVLALEHLKHDIYRLKPNENILLDADGHIALCDFGLSKANLSANATTTWFCGTT 467
Qy 185 PYMAPESSRRKAGYSFVADWMSLGVATYELLGRRPYHRSSTSSKEIIVHTTETTVT 244
Db 468 EYLAPEVLLEDK--GYTKQVDFWSLGVLFEMCGWSPFY---APDVQVMRYNIAFGKVR 522
Qy 245 YP-SAWSEMVSLLKLLPEPDQFQSLSD---VONFPYVNDINWDAVFOKRLIPGP 300
Db 523 FPKGVLSSEGRSFVRGLLRNPNHRLGAVADTTTELKEHPFFADINWDLSSKKVQPPFKP 582
Qy 301 N 301
Db 583 N 583

RESULT 10
T20232
hypothetical protein C54G4.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T20232
R:Wilkinson, J.
submitted to the EMBL Data Library, June 1996
A:Reference number: Z19241
A:Accession: T20232
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-785 <WIL>
A:Cross-references: UNIPROT:Q18846; EMBL:Z75533; PIDN:CAA9814.1; GSPDB:GN00019; CESP:CS54G4
C:Genetics:
A:Gene: CESP:C54G4.1
A:Map position: 1
A:Introns: 55/3; 188/2; 237/2; 339/3; 397/2; 474/3; 504/3; 558/2; 594/3; 687/1; 736/2
C:Superfamily: ribosomal protein S6 kinase II; protein kinase homology

Query Match 24.2%; Score 519.5; DB 2; Length 785;
Best Local Similarity 37.0%; Pred. No. 3.6e-16;
Matches 111; Conservative 72; Mismatches 106; Indels 11; Gaps 8;
Qy 14 ENEDVNFDFEILRAIGKSGFKVCIVQK---NDTKMYAMKYNKQKCVNERE-VRNVP 69
Db 8 EGEKVSMEFNALLRVLGKYGAYKVLVRKVGKGKDHNTIYAMKVLKTRVLTKQKTLHEHTM 67
Qy 70 KELYIQMOGLE-HPFLVNLWYSFQDEEDFMVVDLLGGDLRYHLQONVHFKEETVKLFIC 128
Db 68 AERQVLERLGTFFLVNLFYAFQDTDKLHWVEYVYRGSELTHLCRCHGFLEAARFVIA 127
Qy 129 ELVMAVDYLNQRIIHRDMKPDNILLDEGHVHITDFNIAAM-LPRE-TQITTMAGTKPY 186
Db 128 ELVVAIDSLHQKVIYRDLKLENILLDEGHVKLTDFGLSKLFLPGELDRANSYCGTIEY 187
Qy 187 MAPEMFSSRRKAGYSFVADWMSLGVATYELLGRRPYHRSSTSSKEIIVHTTETTVTY 245
Db 188 MSPEVINRPEG-GYSDVVDWMSLGVISPELLTGCSPFTVDGAQNSKDKIAKRINTMKVPF 246
Qy 246 PSWMSQEMVSLKLLLEPNPQD---FSQSLSDVQFPYVNDINWDAVFOKRLIPGFINKG 303
Db 247 PXTMDVDARDFIGQLEKLEKRLGYNGVDIEKHKFMSSIDWDAVAVKRLKPVIVFRIG 306

RESULT 11
S19027
protein kinase A (EC 2.7.1.1-) catalytic chain - California sea hare
C:Species: Aplysia californica (California sea hare)

C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C:Accession: S19027
R:Bushausen, S.; Bergold, P.; Sturmer, S.; Elste, A.; Roytenberg, V.; Schwartz, J.H.; B
Neuron 1, 853-864, 1988
A:Title: Two catalytic subunits of cAMP-dependent protein kinase generated by alternativ
A:Reference number: S19027; MUID:90166564; PMID:2483106
A:Accession: S19027
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-352 <BSU>
A:Cross-references: UNIPROT:Q16957; EMBL:X63420; NID:G5576; PIDN:CAA45014.1; PID:G5577
as Glu, CTA for residue 271 as Glu, AAC for residue 285 as Asp, and AAC for residue 288
C:Superfamily: kinase-related transforming protein; protein kinase homology
C:Keywords: phosphotransferase
F:42-299/Domain: protein kinase homology <KIN>

Query Match 24.1%; Score 518; DB 2; Length 352;
Best Local Similarity 33.6%; Pred. No. 2.1e-16;
Matches 109; Conservative 83; Mismatches 102; Indels 30; Gaps 10;
Qy 21 DHFEILRAIGKSGFKVCIVQ-KNDTKMYAMKYNKQKCVNERVNVFKELQIMQGLE 79
Db 42 DDPRIKTLGTGSGFVNLVQHKGESRNFYAMKILDKQVVKLQVQVHTLNEKKILQSLN 101
Qy 80 HPFLVNLWYSFQDEEDFMVVDLLGGDLRYHLQONVHFKEETVKLFICELVMAVDYLN 139
Db 102 FPFVLKLEYFQKNSLYMVLFTVGTGEMFSLHRIQFSEPHSRFRFVAAQIVLVLEYLHH 161
Qy 140 QRIIHRDMKPDNILLDEGHVHITDFNIAAMLPRETQITTMAGTKPYMAPEMFSSRRKAG 199
Db 162 LDIMYRLKPNENILLDYSYGLVKVDFGAKVKQRT--WTLCGTPEYLAPEIILSK--G 216
Qy 200 YSFVADWMSLGVATYELLGRRPYHRSSTSSKEIIVHTTETTV---VTYPSAQEMVSL 256
Db 217 YNKAVDWALGVLIYEMAGVPPFF-----ADQPIQIYEKIVSGKVRFPFSHSSDLKDL 270
Qy 257 LKLLLEPNPQFSQL-----SDVQNFYPMNDINWDAVFOKRLIPGFIP-NKGRNLNCDTFF 311
Db 271 LRNLQVLDLTKRFGNLKNGVNDIKNHKWFSTTDIAIYQKRVKVEAPFVPKTKG---AGDTA 327
Qy 312 ELEEMILESPLHKKKRLAKKEK 335
Db 328 NFDD--YEEBPL-----RISSTEX 344

RESULT 12
T21211
hypothetical protein ZK909.2a - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T21211; T28100
R:McLay, K.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z19391
A:Accession: T21211
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-359 <WIL>
A:Cross-references: UNIPROT:P21137; EMBL:Z81511; PIDN:CAB04168.1; GSPDB:GN00019; CESP:ZK909.2a
submitted to the EMBL Data Library, November 1996
A:Reference number: Z20469
A:Accession: T28100
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-359 <WIL>
A:Cross-references: EMBL:Z82096; PIDN:CAB05034.1; GSPDB:GN00019; CESP:ZK909.2a
A:Experimental source: clone ZK909
C:Genetics:
A:Gene: CESP:ZK909.2a
A:Map position: 1

A; Introns: 24/1; 44/3; 87/3; 120/3; 190/3; 318/3
C; Superfamily: kinase-related transforming protein; protein kinase homology

Query Match 24.0%; Score 517; DB 2; Length 359;
Best Local Similarity 33.3%; Pred. No. 2.4e-16;
Matches 110; Conservative 79; Mismatches 119; Indels 22; Gaps 7;

QY 14 ENEDVN---PHEILRAIGKSGFKGKVCIVQKNDTKMYAMKYNKQKCVNERVNF 70
DB 40 ENPAQNTACLDFFRIKTLTGSGRVLVVKHQSNGNYAMKILDKQVVKLQVEHTLN 99
QY 71 ELQIMQGLEHFLVNLWYSFQDEDMFVVDLLGGDLRYHLQONVHFKEETVKLFCEL 130
DB 100 EKRLIQALDFFLVNMFDFKNSNLVNFLEFISGSEMFHLRIGRFPSEPHSRFYAAQI 159
QY 131 VNALDYQONRIHRDMKPDNILLDEGHVHITDFNIA--AMLPRETQITTMAGTKPY 190
DB 160 VLAPEYHLSLDLYRDLKPNLLDSTGYLKITDFGFAKRVKGR--WTLGCTPEYLAPE 217
QY 191 MFSSRKAGYSFVNDWSLGVYAVELLGRPRYHRSSTSSKEIVHTFETTV---VTYPS 247
DB 218 IILSK--GYKAVDWMALGVLIYEMAGYPPFP-----ADQPIQIYEKIVSGVKVFP 268
QY 248 AWSQEMVSLKLLKLEPNDFQFSQ----SDVQNPFPYNDINWDAVFOKRLIPGIPNK 302
DB 269 HFSNELKLLKLLQVLTQKYNLKNGVADIKNHNKWFSGTDWIAIYQKKIEAPFLPKCR 328
QY 303 GRLCDPTFEELMLESKPLHKKKRLAK 332
DB 329 GFGDASNFDDYEEPLRISGTEKCAKEFAE 358

RESULT 13
138556
A; Ribosomal protein S6 kinase 2 (EC 2.7.1.1.-) 3 - human
N; Alternate names: insulin-stimulated protein kinase 1 (PK-1, ISPK1); MAP kinase-activated
C; Species: Homo sapiens (man)
C; Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
C; Accession: I38556; I64835
R; Bjorbaek, C.; Vik, T.A.; Echwald, S.M.; Webb, G.C.; Wang, J.P.; Yang, P.Y.; Vestergaard
Diabetes 44, 90-97, 1995
A; Title: Cloning of a human insulin-stimulated protein kinase (ISPK-1) gene and analysis
nfs.
A; Reference number: I38556; MUID:95113220; PMID:7813820
A; Accession: I38556
A; Status: preliminary; translated from GB/EMBL/DBJ
A; Molecule type: mRNA
A; Residues: 1-740 <BJO>
A; Cross-references: UNIPROT:P51812; EMBL:U08316; NID:G475587; PIDN:AAA81952.1; PID:G4755
R; Moller, D.E.; Xia, C.H.; Tang, W.; Zhu, A.X.; Jakubowski, M.
Am. J. Physiol. 266, 351-359, 1994
A; Title: Human rsk isoforms: cloning and characterization of tissue-specific expression.
A; Reference number: I51901
A; Accession: I64835
A; Status: preliminary; translated from GB/EMBL/DBJ
A; Molecule type: mRNA
A; Residues: 2-423, 'L', 425-479, 'N', 481-493, 495-582 <MOL>
A; Cross-references: GB:L07599; GB:L07601; NID:G401773; PIDN:AAC82495.1; PID:G401774
C; Comment: Although ribosomal protein S6 (see PIR:R3HU6) is phosphorylated by this enzyme
C; Genetics:
A; Gene: GDB:RPS6KA3; RSK; HU-2; RSK2; HU-3
A; Cross-references: GDB:365648; OMIM:300075
A; Map position: Xp22.2-Xp22.2
C; Superfamily: ribosomal protein S6 kinase II; protein kinase homology
C; Keywords: ATP; monomer; phosphoprotein; phosphotransferase; serine/threonine-specific
F; 66-327/Domain: protein kinase homology <KIN>
F; 74-82/Region: protein kinase ATP-binding motif
F; 420-679/Domain: protein kinase homology <KIN2>
F; 428-436/Region: protein kinase ATP-binding motif

Query Match 23.9%; Score 514.5; DB 2; Length 740;
Best Local Similarity 35.8%; Pred. No. 5.7e-16;
Matches 112; Conservative 65; Mismatches 117; Indels 19; Gaps 7;

QY 11 VFDENEDVNFDFEILRAIGKSGFKGKVCIVQK---NDTKMYAMKYNKQKCVNERVNF 67
DB 56 VKEGHEKADPSQFELLKVLGQSGFKGVFLVKKISGDARQLYAMKYLKATLKVDRVRT 115
QY 68 VFKELOIMQGLEHFLVNLWYSFQDEDMFVVDLLGGDLRYHLQONVHFKEETVKLF 127
DB 116 KM-ERDILVEVNHFPVTKLHYAFQTEGKLYLILDLRGDDLTRLKSKVWFTEEDVKFYL 174
QY 128 CELWALDYQONRIHRDMKPDNILLDEGHVHITDFNIA--AMLPRETQITTMAGTKPY 186
DB 175 AELALALDHLHLSGLIYRDLKPNLLDDEGHIKLTDFGLSKESIDHEKKAYSFCGTVEY 234
QY 187 MAPEMFSSRKAGYSFVNDWSLGVYAVELLGRPRYHRSSTSSKEIVHTFETTVTYP 246
DB 235 MAPEVNVNR---GHTQSDAWWSFGVLMPEMLATGLTFP---QGGDKRETMTILKAKLGMP 288
QY 247 AWSQEMVSLKLLKLEPNDFQFSQ----LSDVQNPFPYNDINWDAVFOKRLIPGIPNK 302
DB 289 QFLSPAQSLRLMLFKRNPANRLGAGPDGVBEIKRHSFFSTIDWNKLYRREIHPFPKPAT 348
QY 303 GR---LNCDDPTF 311
DB 349 GRPEDITFYFDPPEF 361

RESULT 14
S48986
A; probable protein kinase SCH9 (EC 2.7.1.1.-) - yeast (Saccharomyces cerevisiae)
N; Alternate names: protein YHR205w
C; Species: Saccharomyces cerevisiae
C; Date: 02-Dec-1994 #sequence_revision 02-Dec-1994 #text_change 16-Aug-2004
C; Accession: S48986; S30022; A28429
R; Macri, C.
Submitted to the EMBL Data Library, February 1994
A; Description: The sequence of S. cerevisiae cosmid 9177.
A; Reference number: S46671
A; Accession: S48986
A; Molecule type: DNA
A; Residues: 1-823 <MAC>
A; Cross-references: UNIPROT:P11792; EMBL:U00029; NID:G551322; PIDN:AA869735.1; PID:G4589
R; di Biasi, F.; Carra, E.; de Vendittis, E.; Masturzo, P.; Burderi, E.; Lambrinoudaki, I.
Yeast 9, 21-32, 1993
A; Title: The SCH9 protein kinase mRNA contains a long 5' leader with a small open reading
frame.
A; Reference number: S30021; MUID:93182531; PMID:8442384
A; Accession: S30022
A; Status: nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 'M', 1-823 <DIB>
A; Cross-references: EMBL:X57629; NID:G5277; PIDN:CAA40853.1; PID:G5279
A; Note: The nucleotide sequence was submitted to the EMBL Data Library, February 1991
R; Toda, T.; Cameron, S.; Sasse, P.; Wigler, M.
Genes Dev. 2, 517-527, 1988
A; Title: SCH9, a gene of Saccharomyces cerevisiae that encodes a protein distinct from,
A; Reference number: A28429; MUID:88255839; PMID:3290050
A; Accession: A28429
A; Molecule type: DNA
A; Residues: 'M', 1-364, 'S', 366-749, 'K', 751-823 <TOD>
A; Cross-references: EMBL:X12560; NID:G4425; PIDN:CAA31073.1; PID:G4426
C; Genetics:
A; Gene: SGD:SCH9
A; Cross-references: SGD:S0001248; MIPS:YHR205w
A; Map position: 8R
C; Superfamily: protein kinase homology
C; Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F; 409-670/Domain: protein kinase homology <KIN>
F; 417-425/Region: protein kinase ATP-binding motif

Query Match 23.9%; Score 514.5; DB 2; Length 823;
Best Local Similarity 31.5%; Pred. No. 6.3e-16;
Matches 139; Conservative 81; Mismatches 156; Indels 65; Gaps 15;
QY 6 SRKPVDFDE--NEDVNF-----DHFELIRAIGKSGFKGKVCIVQKNDTKQY 49

Db 378 SLKRVDEVVSGDILIKWTYKQTKRHYGQDQEVLELLGKGFQGVYQVKKDTQRIY 437
Qy 50 AMKYNKQKVERNEVRNVFELQIM---QGLEHPFLVNLWYSQDEEDMFVVDLLGG 106
Db 438 AMKVLKSVIYKKEIAHTIGERNILVTASKSPFIVGLKFSQTPDLYLVTDYMSGG 497
Qy 107 DLRVHLQNVHFKEETVKLFCELVMDLYLQNRITHRDMKPDNILLDEHGHVHTDEN 166
Db 498 ELFWHLQREGRFSDRAKFIYAEVLVLALEHLDNDIVTRDUKPNILLDANGNIALCDFG 557
Qy 167 IA-AMLPRETQITTMAGTKPYMAPEMFSSRRKAGYSFAVDMWSLGVTAAYELLRRRYPYHI 225
Db 558 LSKADLXDR--NTFCGTTEVLAPELLDE--TCYTKVDFWLSGLVLFEMCCWSPPF- 612
Qy 226 RSSTSSKEIVHTPTTWTYP-SAWSQEMVSLKLLLEPNPDQRFPSQSD---VONFPYM 281
Db 613 --AENNOVMYQKIAFGKVKFPRDVLSEGRSFVKGLLRNPKHRLGAIDDDGRELRAHPFF 670
Qy 282 NDINWDAVFKLLIPGFIPI---KGRINCPTF-----ELEEMILSKPLHKKKR 329
Db 671 ADIDWEALKOKKIPPPKPHLVSETDTSNFDPEFTTASTSYMNHQPMMTATPL---SPA 727
Qy 330 LAKEKDMRKCDSSQTCILQEHLDVQK-----EPIIFN-----REKVNDRFNK 373
Db 728 MQAKFAGTFVDES---AIDEHVNNKFLQNSYFMEPGSFIPGNPLPDDVDIDDDG 784
Qy 374 RQPNLALEQTKDPQVTVNGMD 394
Db 785 EDINDGFNOEKMNNSHSD 805

RESULT 15

T21212
hypothetical protein ZK909.2b - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T21212; T28101
R;McLay, K.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z19391
A;Accession: T21212
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-375 <WIL>
A;Cross-references: UNIPROT:P21137; EMBL:Z81511; PIDN:CAB04169.1; GSPDB:GNO0019; CESP:ZK909.2b
A;Experimental source: clone F21F12
R;White, S.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z20469
A;Accession: T28101
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-375 <W12>
A;Cross-references: EMBL:Z82096; PIDN:CAB05035.1; GSPDB:GNO0019; CESP:ZK909.2b
A;Experimental source: clone ZK909
C;Genetics:
A;Gene: CESP:ZK909.2b
A;Map position: 1
A;Introns: 24/1; 44/3; 87/3; 120/3; 130/3; 318/3
C;Superfamily: kinase-related transforming protein; protein kinase homology

Query Match 23.9%; Score 514; DB 2; Length 375;
Best Local Similarity 34.7%; Pred. No. 3.3e-16;
Matches 105; Conservative 75; Mismatches 101; Indels 22; Gaps 7;
Qy 14 ENEDVN---FDHFILRAIGKSGFKGKCIQKNDTKQYAMKYNKQKVERNEVRNVFK 70
Db 40 ENPAQNTACLDPDFRIKTLGTSGFGRVNLVKHKGSGNYAMKILDKQVKVKQVEHTLN 99
Qy 71 ELQIMQGLEHPEFLVNLWYSQDEEDMFVVDLLGGDLRVHLQNVHFKEETVKLFCELV 130
Db 100 EKRLQAIIDFPFLVNMFTSFKDNLSNLYMVLEFISGEMFSLHRRIGRFSPEHSRFAAQI 159

Qy 131 VMALDYLQNRITHRDMKPDNILLDEHGHVHTDENIAAMLPRETOITTMAGTKPYMAPE 190
Db 160 VLAPEYLHSLDLIYRDUKPNILLDSTGYLKITDGFAGKRVKGR--WTLCGTPEYLAPE 217
Qy 191 MFSRRKAGYSFAVDMWSLGVTAAYELLRRRYPYHRSSTSSKEIVHTPETTV---VTYPS 247
Db 218 IILSK---GYNKAVDWALGVLIYEMAAGYPPFF-----ADQPIQIYEKIVSGKVKFPPS 268
Qy 248 AWSQEMVSLKLLLEPNPDQRFPSQSD---SDVQNFPMNDINWDAVFKRLIPGFIPIPKG 303
Db 269 HFSNELKDLLKNLLQVLTTRYGNLKNGVADIKNKKWFGSTDMIAIYQKKITPPSPF-SKG 327
Qy 304 RLN 306
Db 328 ESN 330

Search completed: December 17, 2004, 09:28:44
Job time : 41 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 17, 2004, 09:25:19 : Search time 74 Seconds
(without alignments)
3164.561 Million cell updates/sec

Title: US-10-620-845-9

Perfect score: 2151

Sequence: 1 MGNTSRKPPVFEDENEDVNF.....VTNGQMDTGLSETFQTSKVS 407

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 02.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1880	87.4	398	2	QB6GW6 m mus muscu
2	1707	79.4	368	2	Q7TPQ4 mus musculu
3	1527	71.0	396	2	Q6GQ72 xenopus lae
4	1441	67.0	414	2	Q9JXJ8 mus musculu
5	1438.5	66.9	414	2	Q7TMD3 mus musculu
6	1438.5	66.9	414	2	AH58412 mus muscu
7	1434.5	66.7	414	2	Q8C4E0 mus musculu
8	1433.5	66.2	414	2	Q9NY57 mus musculu
9	1419.5	66.0	414	2	Q8IY14 homo sapien
10	1333.5	62.0	488	2	Q9JJG4 mus musculu
11	1333.5	62.0	488	2	Q8QZV4 mus musculu
12	1332.5	61.9	486	2	Q86UX6 homo sapien
13	1186.5	55.2	364	2	Q6UXH3 homo sapien
14	1186.5	55.2	364	2	AAQ88719 homo sapi
15	1142	53.1	369	2	Q86UE1 homo sapien
16	1127.5	52.4	368	2	Q9BGT4 macaca fasc
17	910	42.3	333	2	Q7QFG8 anopheles g
18	852.5	39.6	379	2	Q21483 caenorhabdi
19	835	38.8	166	2	Q8WU08 homo sapien
20	714.5	33.2	700	2	Q9VN23 drosophila
21	684	31.8	367	2	Q96WJ8 blumeria gr
22	595.5	27.7	444	1	KKAC.DICDI
23	561.5	26.1	446	2	Q6PLK2 dictyosteli
24	561.5	26.1	446	2	AA06260 plasmodiu
25	561.5	26.1	735	2	Q8I4W3 plasmodium
26	546	25.4	479	1	PK2.DICDI
27	537.5	25.0	648	1	KAPC.DICDI
28	537.5	25.0	683	2	Q6C936 varrowia li
29	534	24.8	480	2	Q43380 avena sativ
30	533.5	24.8	704	2	Q8FMJ9 candida gla
31	532	24.7	471	1	KP19_ARATH
					Q39030 arabidopsis

32	531	24.7	703	2	O6FN22
33	529.5	24.6	465	1	KPK1_ARATH
34	529.5	24.6	465	2	AA138706
35	529.5	24.6	465	2	AA20205
36	529	24.6	456	2	Q8MYF1
37	528.5	24.6	488	2	O6TQF8
38	528.5	24.6	488	2	AAQ93804
39	528.5	24.6	725	2	Q7RSF6
40	527.5	24.5	465	2	Q8LFC1
41	526	24.5	680	1	YPK1_YEAST
42	524.5	24.4	352	2	Q25115
43	524.5	24.4	648	2	O9TXB8
44	523.5	24.3	522	2	Q9Y777
45	521.5	24.2	352	1	KAPC_DROME
					P12370 drosophila
					O6FN22 candida gla
					P42818 arabidopsis
					AA138706 arabidops
					AA20205 arabidops
					Q8MYF1 dictyosteli
					Q6TQF8 zea mays (m
					AAQ93804 zea mays
					Q7RSF6 plasmodium
					Q8LFC1 arabidopsis
					P12688 saccharomyc
					Q25115 hemientrocyt
					Q9TXB8 dictyosteli
					Q9Y777 metarhizium
					P12370 drosophila

ALIGNMENTS

RESULT 1

ID	QB6GW6	PRELIMINARY;	PRT;	398 AA.
AC	QB6GW6;			
DT	01-MAR-2003 (Tremblrel. 23, Created)			
DT	01-MAR-2003 (Tremblrel. 23, Last sequence update)			
DT	05-JUL-2004 (Tremblrel. 27, Last annotation update)			
DE	Mus musculus 16 days neonate cerebellum cDNA, RIKEN full-length			
DE	enriched library, clone:9630050F05 product:SIMILAR TO SERINE THREONINE			
DE	KINASE 32 homolog (Mus musculus 7 days neonate cerebellum cDNA, RIKEN			
DE	full-length enriched library, clone:A730009C22 product:SIMILAR TO			
DE	SERINE THREONINE KINASE 32 homolog) (Mus musculus adult retina cDNA,			
DE	RIKEN full-length enriched library, clone:A930015B13 product:SIMILAR			
DE	TO SERINE THREONINE KINASE 32 homolog)			
GN	Name=A930015B13Rik;			
OS	Mus musculus (Mouse)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=Cerebellum, and Retina;			
RX	MEDLINE=99279253; PubMed=10349636;			
RA	Carninci P., Hayashizaki Y.;			
RT	"High-efficiency full-length cDNA cloning.";			
RL	Meth. Enzymol. 303:19-44(1999).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=Cerebellum, and Retina;			
RX	MEDLINE=21085660; PubMed=11217851;			
RA	RIKEN FANTOM Consortium;			
RT	"Functional annotation of a full-length mouse cDNA collection.";			
RL	Nature 409:685-690(2001).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=Cerebellum, and Retina;			
RA	The FANTOM Consortium,			
RT	the RIKEN Genome Exploration Research Group Phase I & II Team;			
RL	"Analysis of the mouse transcriptome based on functional annotation of			
RT	60,770 full-length cDNAs.";			
RL	Nature 420:563-573(2002).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=Cerebellum, and Retina;			
RX	MEDLINE=20493374; PubMed=11042159;			
RA	Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,			
RT	Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;			
RL	"Normalization and subtraction of cap-trapper-selected cDNAs to			
RT	prepare full-length cDNA libraries for rapid discovery of new genes.";			
RL	Genome Res. 10:1617-1630(2000).			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=Cerebellum, and Retina;			
RX	MEDLINE=20530913; PubMed=11076861;			

RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura K., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa Y., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum, and Retina;
 RA Fukuda J., Aizawa K., Hanamura T., Arakawa T., Bono H., Carninci P.,
 RA Adachi S., Furuno M., Anemaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirokawa T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai K., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akai H., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 CC -I- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 DR EMBL; AK036266; BAC29366.1; -;
 DR EMBL; AK042599; BAC31302.1; -;
 DR EMBL; AK044474; BAC31941.1; -;
 DR HSP; F31751; IGZK.
 DR MGD; MG1:2442403; A930015B13R1K.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR011009; Kinase like.
 DR InterPro; IPR000961; Pkinase C.
 DR InterPro; IPR000719; Prot kinase.
 DR InterPro; IPR002290; Ser thr kinase.
 DR InterPro; IPR008271; Ser_thr_pkin_AS.
 DR Pfam; PF00069; Pkinase; I.
 DR Pfam; PF00433; Pkinase C; 1.
 DR ProDom; PD000001; Prot kinase; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 398 AA; 46509 MW; 689BCA5B25CF18BB CRC64;

Query Match 87.4%; Score 1880; DB 2; Length 398;
 Best Local Similarity 91.2%; Pred. No. 9e-118;
 Matches 351; Conservative 20; Mismatches 14; Indels 0; Gaps 0;

QY 1 MGANTSRKPPVDEENEDVNFHFEILRAIGKSGFKVCIVQKNDPKQYAMKYNKQKV 60
 DB EMBL; AK044474; BAC31941.1; -;
 1 MGANTSSKAPVDEENEDVNFHFEILRAIGKSGFKVCIVQKNDPKQYAMKYNKQKV 60

QY 61 ERNEVRNVFKELOIQMGLEHPLNVLNYSFQDEEDFMFVVDLLGGDLRYHLQNVHFE 120
 DB EMBL; AK044474; BAC31941.1; -;
 61 ERNEVRNVFKELOIQMGLEHPLNVLNYSFQDEEDFMFVVDLLGGDLRYHLQNVHFE 120

QY 121 ETVKLFICELVVALDYLNQRIIHRDKMPDNILLDEGHVHTIDFNIAAMLPRQITWTM 180
 DB EMBL; AK044474; BAC31941.1; -;
 121 ETVKLFICELVVALDYLNQRIIHRDKMPDNILLDEGHVHTIDFNIAAMLPRQITWTM 180

QY 181 AGTKPYMAPFESSRKGAGYFVDMWSLGVYAYELLGRPRYHIRSTSSKSEIVHTFET 240
 DB EMBL; AK044474; BAC31941.1; -;
 181 AGTKPYMAPFESSRKGAGYFVDMWSLGVYAYELLGRPRYHIRSTSSKSEIVHTFET 240

QY 241 TVVTVPSAQSQBMVSLKLLLEPNQDQESQLSDVONFYPYNDINWDAVFOKRLPGIP 300
 DB EMBL; AK044474; BAC31941.1; -;
 241 TVVTVPSAQSQBMVSLKLLLEPNQDQESQLSDVONFYPYNDINWDAVFOKRLPGIP 300

QY 241 AIVTVPSAQSQBMVSLKLLLEPNQDQESQLSDVONFYPYNDINWDAVFOKRLPGIP 300
 DB EMBL; AK044474; BAC31941.1; -;
 241 AIVTVPSAQSQBMVSLKLLLEPNQDQESQLSDVONFYPYNDINWDAVFOKRLPGIP 300

QY 301 NKGRNLCDPTFELEEMILESPLHKKKRLAKKEKMKRKCDSSTCLLOHLSVQKEFI 360
 DB EMBL; AK044474; BAC31941.1; -;
 301 NKGRNLCDPTFELEEMILESPLHKKKRLAKKEKMKRKCDSSTCLLOHLSVQKEFI 360

QY 361 IFNREKYNRDPNFKQPNLALEQTKD 385
 DB EMBL; AK044474; BAC31941.1; -;
 361 IFNREKYNRDPNFKQPNLALEQTKD 385

RESULT 2
 Q7TPQ4 PRELIMINARY; PRT; 368 AA.
 AC Q7TPQ4
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE A930015B13R1K protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Olfactory epithelium;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L.H., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toehiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Olfactory epithelium;
 RA Strausberg R.;
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
 CC -I- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 DR EMBL; BC055002; AAH55002.1; -;
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:protein-serine/threonine kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR000961; Pkinase C.
 DR InterPro; IPR000719; Prot kinase.
 DR InterPro; IPR008271; Ser_thr_pkin_AS.
 DR Pfam; PF00069; Pkinase; I.
 DR Pfam; PF00433; Pkinase C; 1.
 DR ProDom; PD000001; Prot kinase; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 368 AA; 43313 MW; 0DB7F6977C39BB56 CRC64;

Query Match 79.4%; Score 1707; DB 2; Length 368;
 Best Local Similarity 84.2%; Pred. No. 3.1e-106;
 Matches 324; Conservative 17; Mismatches 14; Indels 30; Gaps 1;

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Qy 1 MGANTSRRKPPVFDENEDVDFHPEILRAIGKSGFGKVCIVOKNDTKKMYAMKYNKQKCV 60
Db 1 MGANTSSKAPVFDENEDVDFHPEILRAIGKSGFGKVCIVAKNDTKKMYAMKYNKQKCV 60

Qy 61 ERNEVRNVFKELQIMOGLHPFLVNLWYSFQDEEDFMFVVDLLGGDLRYHLQONVHFKE 120
Db 61 ERNEVRNVFKELQIMOGLHPFLVNLWYSFQDEEDFMFVVDLLGGDLRYHLQONVHFQ 120

Qy 121 ETVKLFCELVMAIDYLNQORIIHRDKPNDILLDEGHVHTDFNTAAMLPRETQITTM 180
Db 121 DTVKLFCELVMAIDYLNQORIIHRDKPNDILLDEGHVHTDFNTAAMLPRETQITTM 180

Qy 181 AGTKPYMAPWFSSRRKAGYSFAVDWWSLGVATYELLGRPPYHRSSTSSKEIVHTPET 240
Db 158 -----APENFTSRKETGYSFAVDWWSLGVATYELLGRPPYHRSSTSSKEIVNMFET 210

Qy 241 TVVTYPSAWSQEMVSLKLLKLEPNPDQFQSDVQNFPPYMNNDINWDAVFKRLIPGFI 300
Db 211 AIVTYPASQEMVSLKLLKLEPNPDQFQSHLTDIQNFPPYMNWDAVQLKRLIPGFI 270

Qy 301 NKGLNCDPTFELBEEMILESPLHKKKRLAKKEDMKRCDSSQTCLLQEHLDVQKEFI 360
Db 271 TKGLNCDPTFELBEEMILESPLHKKKRLAKKEDMKRCDSSQTCLLQEHLDVQKEFI 330

Qy 361 IFNREKVNDRDFNKRQPNLALEQTKD 385
Db 331 IFNREKVSDFNQRQANLALEQTKN 355

RESULT 3
Q6QG72 PRELIMINARY; PRT; 396 AA.
AC Q6QG72;
RA Strausberg R.L., Felling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.J., Haeh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raba S.A., Locuelli N.A., Peters G.J., Abramson R.D., Mullahy S.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smallos D.E., Schermer A., Schein J.E.,
Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RX MEDLINE=22341132; PubMed=12454917;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus

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initiative."
RT Dev. Dyn. 225:384-391(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RA Klein S., Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; BC072876; AAH72876.1; -.
DR InterPro; IPR011009; Kinase-like.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002290; Ser Thr kinase.
DR InterPro; IPR008271; Ser Thr_kin_AS.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Hypothetical protein; Kinase;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 396 AA; 45626 MW; 991810CE21523F85 CRC64;

Query Match 71.0%; Score 1527; DB 2; Length 396;
Best Local Similarity 75.4%; Pred. No. 3.8e-94;
Matches 288; Conservative 41; Mismatches 47; Indels 6; Gaps 2;

Qy 1 MGANTSRRKPPVFDENEDVDFHPEILRAIGKSGFGKVCIVOKNDTKKMYAMKYNKQKCV 60
Db 1 MGANTSSKTPVCDENEENFNHPEILRAIGKSGFGKVCIVOKNDTKKMYAMKYNKQKCV 60

Qy 61 ERNEVRNVFKELQIMOGLHPFLVNLWYSFQDEEDFMFVVDLLGGDLRYHLQONVHFKE 120
Db 61 ERNEVRNVFKELQIMOGLHPFLVNLWYSFQDEEDFMFVVDLLGGDLRYHLQONVRPTE 120

Qy 121 ETVKLFCELVMAIDYLNQORIIHRDKPNDILLDEGHVHTDFNTAAMLPRETQITTM 180
Db 121 ASVKLYICELALADYLNQSIHRDKPNDILLDEGHVHTDFNTAATLVSKGTKITV 180

Qy 181 AGTKPYMAPWFSSRRKAGYSFAVDWWSLGVATYELLGRPPYHRSSTSSKEIVHTPET 240
Db 181 AGTKPYMAPWFSPRGQICYSFAVDWWSLGVATYELLGRPPYHRSSTATDIVHPT 240

Qy 241 TVVTYPSAWSQEMVSLKLLKLEPNPDQFQSDVQNFPPYMNNDINWDAVFKRLIPGFI 300
Db 241 ATVTYPAWSKEIVSLHLLDRNTERFSSLETIQDPYLSVNDVMDAVLLKLSPEFIP 300

Qy 301 NKGLNCDPTFELBEEMILESPLHKKKRLAKKEDMKRCDSSQTCLLQEHLDVQKEFI 360
Db 301 TKGLNCDPTFELBEEMILESPLHKKKRLAKKEDMKRCDSSQTCLLQEHLDVQKEFI 360

Qy 361 IFNREKVNDRDFNKRQPNLALEQ 382
Db 361 VFNREK---SYSKQ---LAVHQ 376

RESULT 4
Q9JUX8 PRELIMINARY; PRT; 414 AA.
AC Q9JUX8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 25, Last annotation update)
DE Serine/threonine protein kinase.
GN Name=Stk32;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

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Db 121 GTVKLYICELALALEYLRVYHIIHRDKPNDLLDEGHVHTDFTNFIATVLKSGSEKASSM 180
Qy 181 AGTKPYMAPEWFS--SRKGAGYSPAVDWSLGVYATAYELLRRRPHYHRSSTSSKEIVHTF 238
Db 181 AGTKPYMAPEWFS--SRKGAGYSPAVDWSLGVYATAYELLRRRPHYHRSSTSSKEIVHTF 238
Db 181 AGTKPYMAPEWFS--SRKGAGYSPAVDWSLGVYATAYELLRRRPHYHRSSTSSKEIVHTF 238
Qy 239 ETTVTVPYSAWSQEMVSLKLLKLEPNPDQRFSQLSDVQNPFPYMDINWDAVFOKRLIPGF 298
Db 241 KVERVHYSSTWCGMVSLLKLLKLEPNPDQRFSQLSDVQNPFPYMDINWDAVFOKRLIPGF 300
Qy 299 IPNKGRLNCDPTFELEEMILESKEPLHKKKKELAK-KEKDMKCDSSOTCLLQEHLDVSQK 357
Db 301 VPKNGRLNCDPTFELEEMILESKEPLHKKKKELAKHRSRDSSTKDCSPLNGHLQOCLETVRK 360
Qy 358 EPIIFNREKVNDRFNKQPNLALEQTKDPQVTNGQM 393
Db 361 EPIIFNREKLRQ-----QCHNGQL 380
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RESULT 6

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AAH58412
ID AAH58412 PRELIMINARY; PRT; 414 AA.
AC AAH58412;
DT 24-MAY-2004 (TrEMBLrel. 27, Created)
DT 24-MAY-2004 (TrEMBLrel. 27, Last sequence update)
DT 24-MAY-2004 (TrEMBLrel. 27, Last annotation update)
DE Serine/threonine kinase 32B.
GN STK32B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Mouse;
RX MEDLINE=22388257; PubMed=12477937;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinstead J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Mouse;
RX Strausberg R.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC058412; AAH58412.1; -.
KW Kinase.
SQ SEQUENCE 414 AA; 47916 MW; 3C394415790594F3 CRC64;
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Query Match 66.9%; Score 1438.5; DB 2; Length 414;
Best Local Similarity 70.2%; Pred. No. 3.3e-88;
Matches 278; Conservative 36; Mismatches 63; Indels 19; Gaps 3;
Qy 1 MGNTSRKPPVFDNEDVNFHFEILRAIGKSGFKVCIVOKNTDKYAMKYNKOKCV 60
Db 1 MGNHSHKPPVFDNEDVNFHFEILRAIGKSGFKVCIVOKNTDKYAMKYNKOKCV 60
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Qy 61 ERNEVRNVFKELOIMQGLEHPELVNLWYSFQDEDMFMVVDLLGGDLRYHLQONVHPKE 120
Db 61 ERNEVRNVFKELOIMQGLEHPELVNLWYSFQDEDMFMVVDLLGGDLRYHLQONVHPKE 120
Qy 121 ETVKLFICEVLVMDYLNQRIIHRDMKPDNILLDEGHVHTDFTNFIATVLKSGSEKASSM 180
Db 121 GTVKLYICELALALEYLRVYHIIHRDKPNDLLDEGHVHTDFTNFIATVLKSGSEKASSM 180
Qy 181 AGTKPYMAPEWFS--SRKGAGYSPAVDWSLGVYATAYELLRRRPHYHRSSTSSKEIVHTF 238
Db 181 AGTKPYMAPEWFS--SRKGAGYSPAVDWSLGVYATAYELLRRRPHYHRSSTSSKEIVHTF 238
Qy 239 ETTVTVPYSAWSQEMVSLKLLKLEPNPDQRFSQLSDVQNPFPYMDINWDAVFOKRLIPGF 298
Db 241 KVERVHYSSTWCGMVSLLKLLKLEPNPDQRFSQLSDVQNPFPYMDINWDAVFOKRLIPGF 300
Qy 299 IPNKGRLNCDPTFELEEMILESKEPLHKKKKELAK-KEKDMKCDSSOTCLLQEHLDVSQK 357
Db 301 VPKNGRLNCDPTFELEEMILESKEPLHKKKKELAKHRSRDSSTKDCSPLNGHLQOCLETVRK 360
Qy 358 EPIIFNREKVNDRFNKQPNLALEQTKDPQVTNGQM 393
Db 361 EPIIFNREKLRQ-----QCHNGQL 380
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RESULT 7

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Q8C4E0
ID Q8C4E0 PRELIMINARY; PRT; 414 AA.
AC Q8C4E0;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 0 day neonate cerebellum cDNA, RIKEN full-length enriched
DE library, clone:C230053G02 product:serine threonine kinase 32, full
DE insert sequence.
GN Name=Stk32;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning."
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
RN [3]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX The FANTOM Consortium;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
RN [4]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=204939374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes."
RL Genome Res. 10:1617-1630(2000).
RN [5]
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RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; Tissue=Cerebellum;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Onoda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; Tissue=Cerebellum;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozawa T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Satoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AK082468; BAC38500.1; -.
DR HSP; P31751; IGZK.
DR MGD; MGI:1927552; Sck32.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; E:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR00719; Prot kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot kinase; 1.
DR SMART; SM00220; S_TK; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 414 AA; 47884 MW; 9C394364BE19E945 CRC64;

Query Match 66.7%; Score 1434.5; DB 2; Length 414;
Best Local Similarity 69.9%; Pred. No. 6.2e-88;
Matches 277; Conservative 37; Mismatches 63; Indels 19; Gaps 3;

QY 1 MGNTSRKPPVFDNEVDNFDHFEILRAIGKSGFGKVCIVQKNDTKQYAMKYNKQKCV 60
DB 1 MGNHSHKPPVFDNEEYVDFHFOILRAIGKSGFGKVCIVQKNDTKQYAMKYNKQKCV 60

QY 61 ERNEVRNVFKELOIQMOGLEHPPFLNLYSFDQEDMFVVDLLGGDLRYHLQONVHFKE 120
DB 61 ERDEVNRVFRLEQIQMOGLEHPPFLNLYSFDQEDMFVVDLLGGDLRYHLQONVHTE 120

QY 121 ETVKLFICELVMDLYLQNRQIHRDKPDNILLDEGHVHITDFNIAAMLPRETQITTM 180
DB 121 GTVKLYICELALALEYLQRYHIHRDKPDNILLDEGHVHITDFNIAATLVKGEKASSV 180

QY 181 AGTKPYMAPEMFS--SRKAGYSFAVDWWSLGVTAAYELLRGRPHIRSRSSKEIVHTF 238
DB 181 AGTKPYMAPEVQYVDDGPGYSYFVDWWSLGVTAAYELLRGRPHIRSRATPIDILNMF 240

QY 239 ETTVVTVPSANQSWESVLLKLEPNPDQRFQSLSDVQNFPPYMDINWDVAFQKRLIPGF 298
DB 241 KVERVHYSSTWCEGVWSVLLKLLTKDPESRLSSLRDIQSNLYLADMNWDVAFKALMPGF 300
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QY 299 IPNKGRLNCDDPTFELEMIKESPLHKKKRLAK-KEKDMRKCDSSQTCLOEHLDSVOK 357
DB 301 VPKNGRLNCDDPTFELEMIKESPLHKKKRLAKRGRSDTKDSCPLNGHLQOCLETVRK 360

QY 358 EFIFNEKYNRDNFKQPNLALQTKDPPQVNGQM 393
DB 361 EFIFNREKURRQ-----QHNQQL 380

RESULT 8
Q9NY57 PRELIMINARY; PRT; 414 AA.
AC Q9NY57;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Serine/threonine protein kinase.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole brain cdna;
RX MEDLINE=20164328; PubMed=10700184;
RA Ruiz-Perez V.L., Ide S.E., Strom T.M., Lorenz B., Wilson D., Woods K.,
RA King L., Francmano C., Freisinger P., Spranger S., Marino B.,
RA Dallapiccola B., Wright M., Meitinger T., Polymetopoulos M.H.,
RA Goodship J.;
RT "Mutations in a new gene in Ellis-van Creveld syndrome and Weyers
RT acrodermal dysostosis.";
RL Nat. Genet. 24:283-286(2000).
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AJ250839; CAB76471.1; -.
DR HSP; P31751; IGZK.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; E:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR00719; Prot kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot kinase; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 414 AA; 47883 MW; 8FCD58A67EFP09B0E CRC64;

Query Match 66.2%; Score 1423.5; DB 2; Length 414;
Best Local Similarity 72.3%; Pred. No. 3.4e-87;
Matches 269; Conservative 40; Mismatches 60; Indels 3; Gaps 2;

QY 1 MGNTSRKPPVFDNEVDNFDHFEILRAIGKSGFGKVCIVQKNDTKQYAMKYNKQKCV 60
DB 1 MGNHSHKPPVFDNEEYVDFHFOILRAIGKSGFGKVCIVQKNDTKQYAMKYNKQKCV 60

QY 61 ERNEVRNVFKELOIQMOGLEHPPFLNLYSFDQEDMFVVDLLGGDLRYHLQONVHFKE 120
DB 61 ERDEVNRVFRLEQIQMOGLEHPPFLNLYSFDQEDMFVVDLLGGDLRYHLQONVHTE 120

QY 121 ETVKLFICELVMDLYLQNRQIHRDKPDNILLDEGHVHITDFNIAAMLPRETQITTM 180
DB 121 GTVKLYICELALALEYLQRYHIHRDKPDNILLDEGHVHITDFNIAATLVKGAERASSM 180

QY 181 AGTKPYMAPEMFS--SRKAGYSFAVDWWSLGVTAAYELLRGRPHIRSRSSKEIVHTF 238
DB 181 AGTKPYMAPEVQYVDDGPGYSYFVDWWSLGVTAAYELLRGRPHIRSRATPIDILNMF 240

QY 239 ETTVVTVPSANQSWESVLLKLEPNPDQRFQSLSDVQNFPPYMDINWDVAFQKRLIPGF 298
DB 241 KVERVHYSSTWCKGWSVLLKLLTKDPESRVSSLHDIQSVFYLADMNWDVAFKALMPGF 300
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QY 299 IPNKGRLNCDPTFELEEMILESKPLHKKKRLAK-KEKDMRKCDSSQTCLLQEHLDVQK 357
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 358 EFIFNREKVR 369
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 361 EFIFNREKLRR 372

RESULT 9
Q8Y14 PRELIMINARY; PRT; 414 AA.
AC Q8Y14
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Serine/threonine kinase 32B.
GN Name=STK32B;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; BC038238; AM38238.1; -.
DR HSSP; P31751; IGZK.
DR GO; GO:000524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR00719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC_1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 414 AA; 47784 MW; FOE5EE695FA8242F CRC64;
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Query Match

66.0%; Score 1419.5; DB 2; Length 414;

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Best Local Similarity 72.3%; Pred. No. 6.2e-87;
Matches 269; Conservative 39; Mismatches 61; Indels 3; Gaps 2;
QY 1 MGANTGRKPPVFDENEDVDFEILRAIGKSGFKVCIVQKNDTKQYAMKYNKQKCV 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1 MCGNHSHKPPVFDENEDVDFEILRAIGKSGFKVCIVQKNDTKQYAMKYNKQKCI 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 ERNEVRNVKELQIMOGLEHPLVNLWYSFQDEDMVMVVDLLGGDLRVHLOQNVHFK 120
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 ERDEVNRVRELQIMOGLEHPLVNLWYSFQDEDMVMVVDLLGGDLRVHLOQNVHFT 120
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 ETVKLFICELVMAVDLQONRIHRDMKPNILLDEHGHVHITDFNIAAMLPRETQITTM 180
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 GTVKLYICELALALEYLQRYHIIHRDIKPNILLDEHGHVHITDFNIAATVVKGAERASM 180
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 181 AGTKPYMAPEMFS--SRKGAGYFAVDWMSLGVATVELLRGRPPYHTRSTSSKEIVHTF 238
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 181 AGTKPYMAPEVFQVMDGGPGSYVPVDWMSLGVATVELLRGRPPYHTRSTSSKEIVHTF 240
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 239 ETTVTVPYPSAQSQMSVLLKLEPNPDQRFQSDVQNFPMYNDINWDVAFOKRLIPGF 298
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 241 KVERVHYSSTWCKGMVALURKLLTKQPSRVSSLDIQSVYLDAMNDVAFKALMPGF 300
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 299 IPNKGRLNCDPTFELEEMILESKPLHKKKRLAK-KEKDMRKCDSSQTCLLQEHLDVQK 357
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 301 VPNKGRLNCDPTFELEEMILESKPLHKKKRLAKNRSRDGKSCPLNGHLQHCLETVRE 360
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 358 EFIFNREKVR 369
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 361 EFIFNREKLRR 372

RESULT 10
Q9JJG4 PRELIMINARY; PRT; 488 AA.
AC Q9JJG4
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus brain cDNA, clone MNCB-1563, similar to AJ250840
DE serine/threonine protein kinase (Mus musculus).
GN Name=Pkek;
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL;
RA Osada N., Kusuda J., Tanuma R., Ito A., Hirata M., Sugano S.,
RA Hashimoto K.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AB041542; BAA95027.1; -.
DR HSSP; P31751; IGZK.
DR MGD; MGI:2385336; Pkek.
DR GO; GO:000524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR00719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC_1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 488 AA; 55276 MW; 310483FF69E24E39 CRC64;
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DR GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR001009; Kinase-like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR008271; Ser_thr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW ATP-binding; Hypothetical protein; Kinase;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 488 AA; 5562 MW; 286A927BB6B78EF2 CRC64;

Query Match 62.0%; Score 1333.5; DB 2; Length 488;
Best Local Similarity 63.3%; Pred. No. 4.3e-81;
Matches 255; Conservative 56; Mismatches 83; Indels 9; Gaps 3;

QY 6 SRKPPVDFEDVDFHFEILRAIGKSGFGKVCIVQKNDTKMYAMKYNKQKCV 65
DB 77 SARPPVDFDKEDVDFHFEILRAIGKSGFGKVCIVQKNDTKMYAMKYNKQK 136
QY 66 RNVFKEIQMOGLHPPFLVNLWYSFQDEDMFMVVDLLGGDLRYHLQONVH 125
DB 137 RNVFREILQIEHVFVNLWYSFQDEDMFMVVDLLGGDLRYHLQONVH 196
QY 126 FICELVMDLYLQRIHHRDKPDNILLDEGHVHITDFNIAALPRETQITMAG 185
DB 197 YICEMALDLYRSQHIIHRDVKPDNILLDQGHVHITDFNIAALPRETQIT 256
QY 186 YMAPDEMSS--RKAGYSFADVWSLGVTAELLGRPRPHIRSRSTSSKEIVH 243
DB 257 YMAPEIFHFSFNGGTGYSFEVDWWSVGMAYELLRGWRPYDIHSSNAVES 316
QY 244 TYPASQEWVSLKLEPNPDQRFQSLSDVQNPFPYMDINWDVAFQKRLPGFI 303
DB 317 QYVPTWSKEMVALLKLTVPNPEHRSFSLQDMQAPSLAHVWDLSEKVP 376
QY 304 RLNCDDPTFELEEMILESPLHKKKRLAKKEDKMRKCDSSQT--CLLQEHLS 361
DB 377 RLHCDDPTFELEEMILESPLHKKKRLAKKEDKMRKCDSSQT--CLLQEHLS 436
QY 362 FNRKVRNDRKNRPNALAQTKDPQVTVNGQMTGLSETFQTS 404
DB 437 FNRKVL-----KRSQELMSEPPPGPETSMDTSDTADSEAPTA 474

RESULT 12
Q86UX6 PRELIMINARY; PRT; 486 AA.
AC Q86UX6;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE PKE protein kinase.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RA Ma A.-H., Nelson D.A., Xia L., Ravi L., Chen H.-C., Robinson D.R.,
RA Kung H.-J.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AY098866; AA021719.1; -
DR HSSP; P31751; 1GZK.
DR GO:0005524; F:ATP binding; IEA.
DR GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO:0016740; F:transferase activity; IEA.
DR GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR001009; Kinase-like.

DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR008271; Ser_thr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 486 AA; 54994 MW; 38FEFBB3863B21E3 CRC64;

Query Match 61.9%; Score 1332.5; DB 2; Length 486;
Best Local Similarity 65.0%; Pred. No. 5e-81;
Matches 253; Conservative 55; Mismatches 76; Indels 5; Gaps 3;

QY 1 MGATSRKPPVDFEDVDFHFEILRAIGKSGFGKVCIVQKNDTKMYAMKYNKQKCV 60
DB 72 MSATARR--PVFDDKEDVDFHFEILRAIGKSGFGKVCIVQKNDTKMYAMKYNKQ 130
QY 61 ERNEVRNVFKEIQMOGLHPPFLVNLWYSFQDEDMFMVVDLLGGDLRYHLQONVH 120
DB 131 ERDEVRNVFKEIQMOGLHPPFLVNLWYSFQDEDMFMVVDLLGGDLRYHLQONVH 190
QY 121 ETVKLFICELVMDLYLQRIHHRDKPDNILLDEGHVHITDFNIAALPRETQIT 180
DB 191 DTVRLYICEMALDLYLRGQHIHHRDVKPDNILLDEGHVHITDFNIAALPRET 250
QY 181 AGTKPYMAPDEMSS--RKAGYSFADVWSLGVTAELLGRPRPHIRSRSTSSKEIVH 238
DB 251 AGTKPYMAPDEMSS--RKAGYSFADVWSLGVTAELLGRPRPHIRSRSTSSKEIVH 310
QY 239 ETTVVTYPSAWSQEWVSLKLEPNPDQRFQSLSDVQNPFPYMDINWDVAFQKRL 298
DB 311 STVSQVQVPTWSKEMVALLKLTVPNPEHRSFSLQDMQAPSLAHVWDLSEKVP 370
QY 299 IPNKGRLNCDDPTFELEEMILESPLHKKKRLAKKEDKMRKCDSSQT--CLLQEHLS 356
DB 371 VPNGRLHCDDPTFELEEMILESPLHKKKRLAKKEDKMRKCDSSQT--CLLQEHLS 430
QY 357 KEFTIFNREKVRNDRKNRPNALAQTKD 385
DB 431 QDFVIFNREKVRNDRKNRPNALAQTKD 459

RESULT 13
Q6UXH3 PRELIMINARY; PRT; 364 AA.
AC Q6UXH3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE HSA250839.
GN ORPNames-UNQ3003;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vanden R., Watanabe C., Wieda D., Woods K., Xie M.H., Yaneura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
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RL Genome Res. 13:2265-2270(2003).
CC -I- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AY358353; AAQ88719.1; -.
DR InterPro; IPR011009; Kinase_like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR008271; Ser_thr_kin_AS.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00069; PKinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 364 AA; 42195 MW; F552D0CB54C7A27C CRC64;

Query Match 55.2%; Score 1186.5; DB 2; Length 364;
Best Local Similarity 69.9%; Pred. No. 2.1e-71;
Matches 225; Conservative 38; Mismatches 56; Indels 3; Gaps 2;

QY 51 MKYMNKQKCVNERNVFKEIQIMQGLEHPLVNLWYSFQDEEDMFVVDLLGGDLRY 110
DB 1 MKYMNKQKCIERDEVNRVFRLEIQIMQGLEHPLVNLWYSFQDEEDMFVVDLLGGDLRY 60

QY 111 HLQONVHFKEETVKLFICELVMALDYLNQRIIHRDKPDNILLDEGHVHITDFNIAAM 170
DB 61 HLQONVHFTEGVTKVYICELALALEYLQRYHIIHRDKPDNILLDEGHVHITDFNIAV 120

QY 171 LPRETQITTMAGTKPYMAPEMPS--SRKGAGYSFVADWWSLGVTAPELLRGRPPYHRS 228
DB 121 VKGAERASSMAGTKPYMAPEVFQVYMDRPGVSYFVDMWSLGITAYELLRGRPPYHRSV 180

QY 229 TSKEIIVHTFTVTVTYPSAQSQEMVSLKLLLEPNPDQSFQSDVQNFPMYNDINWDA 288
DB 181 TPDEILNMFKVERVHYSTWCKGMVALLKLLTKDPESRVSSLDHIOQSVPLADMWDA 240

QY 289 VFQKRLIPGIPNKGRLNCDPTFELEEMILESPLHKKKKRLAK-KEKDMRKCDSSQTCL 347
DB 241 VFKKALMPGFPVNGRLNCDPTFELEEMILESPLHKKKKRLAKNRSRDTGDKSCPLNGH 300

QY 348 LQEHLSVQKEFIIFNREKNR 369
DB 301 LQHCLETVREEFIFNREKLRR 322

RESULT 15
Q86UE1 PRELIMINARY; PRT; 369 AA.
ID Q86UE1
AC Q86UE1; 2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE PKE protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshitoki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahay J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalls D.B., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;

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RL Genome Res. 13:2265-2270(2003).
CC -I- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AY358353; AAQ88719.1; -.
DR InterPro; IPR011009; Kinase_like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR008271; Ser_thr_kin_AS.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00069; PKinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 364 AA; 42195 MW; F552D0CB54C7A27C CRC64;

Query Match 55.2%; Score 1186.5; DB 2; Length 364;
Best Local Similarity 69.9%; Pred. No. 2.1e-71;
Matches 225; Conservative 38; Mismatches 56; Indels 3; Gaps 2;

QY 51 MKYMNKQKCVNERNVFKEIQIMQGLEHPLVNLWYSFQDEEDMFVVDLLGGDLRY 110
DB 1 MKYMNKQKCIERDEVNRVFRLEIQIMQGLEHPLVNLWYSFQDEEDMFVVDLLGGDLRY 60

QY 111 HLQONVHFKEETVKLFICELVMALDYLNQRIIHRDKPDNILLDEGHVHITDFNIAAM 170
DB 61 HLQONVHFTEGVTKVYICELALALEYLQRYHIIHRDKPDNILLDEGHVHITDFNIAV 120

QY 171 LPRETQITTMAGTKPYMAPEMPS--SRKGAGYSFVADWWSLGVTAPELLRGRPPYHRS 228
DB 121 VKGAERASSMAGTKPYMAPEVFQVYMDRPGVSYFVDMWSLGITAYELLRGRPPYHRSV 180

QY 229 TSKEIIVHTFTVTVTYPSAQSQEMVSLKLLLEPNPDQSFQSDVQNFPMYNDINWDA 288
DB 181 TPDEILNMFKVERVHYSTWCKGMVALLKLLTKDPESRVSSLDHIOQSVPLADMWDA 240

QY 289 VFQKRLIPGIPNKGRLNCDPTFELEEMILESPLHKKKKRLAK-KEKDMRKCDSSQTCL 347
DB 241 VFKKALMPGFPVNGRLNCDPTFELEEMILESPLHKKKKRLAKNRSRDTGDKSCPLNGH 300

QY 348 LQEHLSVQKEFIIFNREKNR 369
DB 301 LQHCLETVREEFIFNREKLRR 322

RESULT 14
AAQ88719 PRELIMINARY; PRT; 364 AA.
ID AAQ88719
AC AAQ88719; 2003 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE HSA250839.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primata; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC PubMed=12975309;
RX Clark H.P., Gurney A.I., Abaya E., Baker K., Baldwin D., Bruch J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu O., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seehagiri S., Simmons L., Singh J., Smith Y., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wiand D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
RT Effort to Identify Novel Human Secreted and Transmembrane Proteins: A

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Strausberg R.;
RA Submitted (JAN-2003) to the EMBL/GenBank/DBDJ databases.
CC -i- SIMILARITY: Belongs to the Ser/thr protein kinase family.
DR HMBL; BC045760; AAH45760.1; -.
DR HSSP; O15530; 1H1W.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006488; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase_like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 369 AA; 42395 MW; E152C66BB2D786B4 CRC64;

Query Match 53.1%; Score 1142; DB 2; Length 369;
Best Local Similarity 63.2%; Pred. No. 2e-68;
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Qy 48 MYAMKYNKQKQVERNEVNFKEIQMGLHPFLVNLWYSFQDEDMFVVDLLCGD 107
Db 1 MYAMKYNKQKQCIERDEVNFRELEILQIEHVFLVNLWYSFQDEDMFVVDLLCGD 60

Qy 108 LRYHLQNVHPKBTVKLFICELVNLQYQRIIHRDMKPDNILLDEHGHVHTDFNI 167
Db 61 LRYHLQNVQPSQEDTVRLYICEMALDYLGRQHIHRDVKPDNILLDERGHAHTDFNI 120

Qy 168 AAMLPRETOITTMAGTKPYMAPEMPSS--RYGAGYSFVDMWSLGVTAAYELLGRPPYHI 225
Db 121 ATIIKGERATALAGTKPYMAPETPFHSFVNGGTGYSEVDWWSVGMAYELLGRPPYDI 180

Qy 226 RSSTSSKEIVHTFTTVVTPSAQSEMVSLKKLEPNPDPFQSDVQNFPMNDIN 285
Db 181 HSSNAVSLVQLFSTVSQYVPTWSKENVALLRKLAVNPEHRLSSLDQVQAAPALAGVL 240

Qy 286 WDAVFQKRLIPGFIPNKGRLNCDPTFELEEMILESPLHKKKKGLAKKDKMRKCDSSQT 345
Db 241 WDLSEKRVPEPGFVFNKGRGLHCDPTFELEEMILESRLHKKKKGLAKKSRDNRDSSQS 300

Qy 346 --CLIQEHLDSVQKEFIIFNREKVNDRDNKQPNLALAEQTKD 385
Db 301 ENDYLOQCLDAIQODFVIFNREKLKRSQDLPREPLPAPESRD 342

Search completed: December 17, 2004, 09:26:44
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